120 Sequence Protocol

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: metaGen Gesellschaft für Genomforschung
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TEDEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674
- (ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Normal Bladder Tissue
- (iii) Number of sequences: 365
- (iv) COMPUTER-READABLE FORM:
 - (A) MEDIUM TYPE: \Floppy disk

 - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)
- (2) INFORMATION ON SEQ ID NO. 1:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1722 base paiks

 - (B) TYPE: Nucleic acid (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

cgttgaagta gatgcacaac agtgtatgct tgaaatcttg gatactgcag gaacggagca 60 atttacagca atgagggatt tatacatgaa aaatggacaa ggatttgcat tagtttattc 120 catcacagca cagtccacat ttaacgattt acaagacctg agagaacaga ttcttcgagt 180 taaagacact gatgatgttc caatgattct tgttggtaat aagtgtgact tggaagatga 240 aagagttgta gggaaggaac aaggtcaaaa tctagcaaga caatggaaca actgtgcatt 300 cttagaatct tctgcaaaat caaaaataaa tgttaatgag atcttttatg acctagtgcg 360 gcaaattaac agaaaaactc cagtgcctgg gaaggctcgc aaaaagtcat catgtcagct 420 gctttaatat actaaatgca ttgtagctct gagccaggtc tgaagaactg ttgcccaatt 480 caacagtgcc agcattccaa ctttgttaaa cctaccaaca tcttaaaatgg actttcctgt 540 ggtggtaccc tttaagaggc ggatgaaagc tactatatca gtttgcacat tctaatcact 600 ttccagtatc acaagagaga tttttactta tataatagtc ctagagtttg cagctggtaa 660 aaccagagge tacatecagt attactgeta agagacatte tteatecace aatgttgtae 720 atgtatgaaa atggtgtact gtatacttta acatgcccca tactttgtat tggagagtac 780 aataatgtaa atcctaaaag caccactatt ttagcataat aaaagaaagt ccaaagagct 840 octatataga ctactocaga taacttogot totttgatac ttgtagotta ttgtaatttt 900 ttttaagaaa ttcaaggtca ttattattgt acaaaataag cgctttgatt aacacagcta 960 tatagttttt ttaattttta aaaaacctgt ggagacggtg atcttgtctt taaaacatga1020 tagtcctttc agtataatgt cttagattaa agacgttgcc tttaatatct gttgggaagg1080 aaatgtccag acttttcaaa tctcttatta tatgtttcct ttttttgttt acatagggaa1140 caatgtttat agtcgtgtgt acagtggggg tctacaacaa gaagtgtata ttttcaaaca1200 attititaat gatttaacaa tiittigtaaa toattitoag gottotgoag otgtagatto1260 tcactgtgaa tcccttgctt gctcatgcat aagtgtattt gcaataccaa atatacaggt1320 ttagtatttt tgcctgttag tgattgtttc acatgtgtaa cgttttggtt gagatgttaa1380 atggtggacg agtactgtgg atgtgaatgt gggaagtaat tttaatcata tgtaattggt1440 cacaaggeet aattigeagt aactatiget gittiatita acaatgeett gitgettigt1500 atgcattaat gtttggatgt aaagattgtg tgtctatcca acagggagcc acagtattta1560 aattgaccaa cctaatgtta caactacttt gaggtggcca atgtaaact aaaagcctta1620 attaaagtgg tgcaattttg tataacttag catcagtagt tcaataaatt tggattgcca1680 tgcaagggct tgcattataa aaaaaaaaaaa aa

(2) INFORMATION ON SEQ ID NO. 2:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1187 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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qqccaccqqc cqqctqcaca cqacttcccc ctqqqqcqqc actccccaqc aggactaccc 120
egaccetggg tettgaggaa gtgetgagea geagggaetg teaccetgee etgeegette 180
ctcccqqctt ccatccccac ccqqqqccca attacccatc cttcctqccc gatcagatqc 240
ageogeaagt ecogoogete cattaceaag ageteatgee accoggttee tgeatgeeag 300
aggageccaa gecaaagagg ggaagaegat egtggeeceg gaaaaggaee gecaeccaca 360
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ttttactttt cacactgtct tcccgatgag ggaaggagcc cagccagaaa gcactacaat 720
catggtcaag tteccaactg agtcatcttg tgagtggata atcaggaaaa atgaggaatc 780
caaaagacaa aaatcaaaga acagatgggg totgtgactg gatottotat cattocaatt 840
ctaaatccga cttgaatatt cctggactta caaaatgcca agggggtgac tggaagttgt 900
ggatatcagg gtataaatta tatccgtgag ttgggggagg gaagaccaga attcccttga 960
attgtgtatt gatgcaatat aagcataaaa gatcaccttg tattctcttt accttctaaa1020
agecattatt atgatgttag aagaagaga agaaattcag gtacagaaaa ccatgtttaa1080
atagectaat gatggtgttt gtgagettgg teetaaaggt eecaacaagg gagecaaagg1140
tttaaactgc tggatccttg gcaaggggaa atctgtgttt ttttccg
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(2) INFORMATION ON SEQ ID NO. 3:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1478 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

gegaaceege gegetgeeeg gteetgeget geecageggg aggggetgga eecegegtte 60 ctcctccctg ccggtcccca tccttaaagc gagagtctgg acgccccgcc tgtgggagag 120 agegeeggga teeggaeggg gageaacegg ggeaggeegt geeggetgag gaggteetga 180 ggctacagag ctgccgcggc tggcacacga gcgcctcggc actaaccgag tgttcgcggg 240 ggctgtgagg ggagggcccc gggcgccatt gctggcggtg ggagcgccgc ccggtctcag 300 cocgeceteg getgetetee tecteegget gggagggee gtageteggg geogtegeea 360 gccccggccc gggctcgaga atcaagggcc tcggccgccg tcccgcagct cagtccatcg 420 ccettgccgg gcagcccggg cagagaccat gtttgacaag acgcggctgc cgtacgtggc 480 cctcgatgtg ctctgcgtgt tgctggctgg attgcctttt gcaattctta cttcaaggca 540 tacccccttc caacgaggag tattctgtaa tgatgagtcc atcaagtacc cttacaaaga 600 agacaccata cottatgogt tattaggtgg aataatcatt coattcagta ttatogttat 660 tattettgga gaaaccetgt etgittaetg taacetttig cacteaaatt cetttateag 720 gaataactac atagccacta tttacaaagc cattggaacc tttttatttg gtgcagctgc 780 tagtcagtcc ctgactgaca ttgccaagta ttcaataggc agactgcggc ctcacttctt 840 ggatgtttgt gatccagatt ggtcaaaaat caactgcagc gatggttaca ttgaatacta 900 catatytcga gggaatycag aaagagttaa ggaaggcagg ttgtccttct attcaggcca 960 ctcttcgttt tccatgtact gcatgctgtt tgtggcactt tatcttcaag ccaggatgaa1020 gggagactgg gcaagactct tacgccccac actgcaattt ggtcttgttg ccgtatccat1080 ttatgtgggc ctttctcgag tttctgatta taaacaccac tggagcgatg tgttgactgg1140 acticational ggagoticting tigicalitatic agricultural tatiguaticing atticiticaal 200 agaaagaact tcttttaaag aaagaaaaga ggaggactct catacaactc tgcatgaaac1260 accaacaact gggaatcact atccgagcaa tcaccagcct tgaaaggcag cagggtgccc1320 aggtgaaget ggeetgtttt etaaaggaaa atgattgeea caaggeaaga gggatgeate1380 tttcttcctg ggtgtacaag cccttttaaa gaccttctgc tggctgcgat gcctcttgga1440 atgcacagtt gtgtgtaaca gagttacctt aactcgtg

- (2) INFORMATION ON SEQ ID NO. 4:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

gccacattte eggggttttg egggeeege gatgtttee agagetttte aagtgggaag 60 aggagagega caacgtgaaa atgeeeegtg eeggggegte eaceggagte etgeeagetg120 teeggegetg gggtggaegt etgatttatg aageteecea teeacetate tgagtacetg180 actteteagg actgaeacet acageateag gtacacaget teteetagea tgaettegat240 etgateagea aacaagaaaa tttgteteee gtagttetgg ggegtgttea eeacetacaa300 eeacagaget gteatggetg eeatetetae tteeateeet gtaattteae ageeeeagtt360 eacageeatg aatgaaeea agtgetteta eaacgagtee attgeettet t

(2) INFORMATION ON SEQ ID NO. 6:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3181 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

cgggtggggt gggagcaggg ggggacagtg ccccgggaac ccggtgggtc acacacacgc 60 actgcgcctg tcagtagtgg acattgtaat ccagtcggct tgttcttgca gcattcccgc 120 tecetteeet ecatagecae getecaaace ecagggtage catggeeggg taaageaagg 180 gccatttaga ttaggaaggt ttttaagatc cgcaatgtgg agcagcagcc actgcacagg 240 aggaggtgac aaaccatttc caacagcaac acagccacta aaacacaaaa agggggattg 300 ggcggaaagt gagagccagc agcaaaaact acattttgca acttgttggt gtggatctat 360 tggctgatct, atgcctttca actagaaaat tctaatgatt ggcaagtcac gttgttttca 420 ggtccagagt agtttctttc tgtctgcttt aaatggaaac agactcatac cacacttaca 480 attaaggtca agcccagaaa gtgataagtg cagggaggaa aagtgcaagt ccattatgta 540 atagtgacag caaagggacd aggggagagg dattgddttd totgdddada gtot .cog- 600 gtgattgtct ttgaatctga atcagccagt ctcagatgcc ccaaagtttc ggttcctatg 660 agcccggggc atgatctgat ccccaagaca tgtggagggg cagcctgtgc ctgcctttgt 720 gtcagaaaaa ggaaaccaca gtgagcctga gagagacggc gattttcggg ctgagaaggc 780 agtagttttc aaaacacata gttaaaaaag aaacaaatga aaaaaatttt agaacagtcc 840 agcaaattgc tagtcagggt gaattgtgaa attgggtgaa gagcttagga ttctaatctc 900 atgttttttc cttttcacat ttttaaaaga acaatgacaa acacccactt atttttcaag 960 gttttaaaac agtctacatt gagcatttga aaggcgtgct agaacaaggt ctcctgatcc1020 gtccgagget getteccaga ggageagete tececaggea tttgccaagg gaggeggatt1080 tecetggtag tgtagetgtg tggettteet teetgaagag teegtggttg ceetagaace1140 taacaccccc tagcaaaact cacagagett teegtttttt tettteetgt aaagaaacat1240 ttcctttgaa cttgattgcc tatggatcaa agaaattcag aacagcctgc ctgtcccccc1260 qcacttttta catattttg tttcatttct gcagatggaa agttgacatg ggtggggtgt1320 ccccatccag cgagagagtt tcaaaagcaa aacatctctg cagtttttcc caagtaccct1380 gagatacttc ccaaagccct tatgtttaat cagcgatgta tataagccag ttcacttaga1440 caactttacc cttcttgtcc aatgtacagg aagtagttct aaaaaaaatg catattaatt1500 tettececca aageeggatt ettaattete tgeaacaett tgaggacatt tatgattgte1560 cctctgggcc aatgcttata cccagtgagg atgctgcagt gaggctgtaa agtggccccc1620 tgcggcccta gcctgacccg gaggaaagga tggtagattc tgttaactct tgaagactcc1680 agtatgaaaa tcagcatgcc cgcctagtta cctaccggag agttatcctg ataaattaac1740 ctctcacagt tagtgatcct gtccttttaa cacctttttt gtggggttct ctctgacctt1800 tcatcgtaaa gtgctgggga ccttaagtga tttgcctgta attttggatg attaaaaaat1860 gtgtatatat attagctaat tagaaatatt ctacttetet gttgtcaaac tgaaattcag1920 agcaagttcc tgagtgcgtg gatctgggtc ttagttctgg ttgattcact caagagttca1980 gtgctcatac gtatctgctc attttgacaa agtgcctcat gcaaccgggc cctctctctg2040 eggeagagte ettagtggag gggtttacet ggaacattag tagttaceae agaataegga2100 agagcaggtg actgtgctgt gcagctctct aaatgggaat tctcaggtag gaagcaacag2160 cttcagaaag agctcaaaat aaattggaaa tgtgaatcgc agctgtgggt tttaccaccg2220 totgtotcag agtoccagga cottgagtgt cattagttac tttattgaag gttttagacc2280 catagoaget ttgtctctgt cacatoagea atttcagaac caaaagggag gctctctgta2340 ggcacagage tgcactatca cgageetttg ttttteteca caaagtatet aacaaaacca2400 atgtgcagac tgattggcct ggtcattggt ctccgagaga ggaggtttgc ctgtgatttc2460 ctaattatcg ctagggccaa ggtgggattt gtaaagcttt acaataatca ttctggatag2520 agtcctggga ggtccttggc agaactcagt taaatctttg aagaatattt gtagttatct2580 tagaagatag catgggaggt gaggattoca aaaacatttt atttttaaaa tatcctgtgt2640 aacacttggc tottggtacc tgtgggttag catcaagttc tococagggt agaattcaat2700 cagageteca gittgeatti ggatgigtaa attacagtaa teecattice caaacetaaa2760 atctgttttt ctcatcagac tctgagtaac tggttgctgt gtcataactt catagatgca2820 ggaggctcag gtgatctgtt tgaggagagc accctaggca gcctgcaggg aataacatac2880 tggccgttct gacctgttgc cagcagatac acaggacatg gatgaaattc ccgtttcctc2940 tagtitette etgtagtaet eetettitag ateetaagte tettacaaaa getitgaata3000 ctgtgaaaat gitttacatt ccatttcatt tgtgttgttt ttttaactgc attttaccag3060 atgttttgat gttatcgctt atgttaatag taattcccgt acgtgttcat tttattttca3120 tgctttttca gccatgtatc aatattcact tgactaaaat cactcaatta atcaataaaa3180 3181

(2) INFORMATION ON SEQ ID NO. 7:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1964 base pairs

 - (B) TYPE: Nucleic acid (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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					ggccctcgcg	
					cccgcctata	
					atgacacago	
						360
	cagcagttac					420
	gcagatggga					
					atgaacgctg	540
	caagcagtca					
					aaccagagaa	
					tctttggttt	
	ttagaaaacc				~	720
ggttttcttc	acaatcttga	acattttaca	gtagaactca	tctaaaaatg	gatttgggga	780
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caggaaaatg	cttctccttt	taaaatcccc	tccactcctc	acacacacac	acctcttgaa!	1140
accettecee	aagaatgttt	ctttatagac	ggacttcatt	gaaatctttg	ttgttcttga:	1200
atcaagtgta	atataatttt	tttcttcttt	tttaaaatat	tcccactcag	cactcagaga:	1260
cacaaaaata	ctgtaagtct	caattaacag	cagaatctca	gagaaaagct	gtttgcaatc:	1320
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gataaaactc	aaatagcagt	ccccagtgat	ttgcctctta	ggttctttct	taaattgttg:	1560
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					cctgagttca:	
tecectgtga	atcagagtgc	acaagcacct	ctcctgtgag	tggctaatga	gaagagggac.	1800
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					attctcttcc:	
	tccagggata					1964

(2) INFORMATION ON SEQ ID NO. 8:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1702 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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caqttctqca ggtcctqact ctqcaqaqqq aaqaqqcaqa aaqaqaqaaa ctqtcaqaqt 420
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aaattttcat gtotttaaat accouttggt aagttgotto tgaagocagt gggggotoot 540
cagatagaga ggttcccctt tcaaatccca gtgccgctct gttctctttc cttcccctcc 600
cacteceet ettetteete tgtagagatg caagaaattg etgteecata aaaateataa 660
ttgcagtagc taaagctggg gtcacttcgt gaattcacca gagactcaaa gatcttttat 720
tggctctggg ctgtgctcag tgtctttggc ctcagagaac aacttgaatg acttcctggt 780
ttcctggcat aaattattcc tggtgagaca tgtggcttaa ctcacaggtt tcccatcagc 840
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ggatttggag ctccgaggca gtaataactg aacaagcagc cctgtcccct aggctgcaga1020
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cccaactgca tgcaaaagac caccatcctc agaagccaag ttgtctttta tgaagaggcall40
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aactecttgt atgtgtgcta aaaccaggga agcatgtgac tgccaagcag gcaacccctg1260
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tettecetee tgtggaateg aggggaaatt attetteeea atacettgat ttgattttca1380
gtttcataag cttcttcctc tgaatcttat tgagggacta tggtaccaag caggtaggac1440
tqttcacctg gtggaacagt tcttgctctg ccttctaggc ttcatcccag aaatccagcc1500
tetttetgga gaccecaaag etggagggag atgggettte etettgggeet etetteetae1560
tttgccatcc acactgctcc tggctaaccc cagcaagaac caacaaatgg gtagggaagc1620
cccatctaat tggctttttt tcttcaatta tggacgtgca ttgttttggt tgggaacaaa1680
aggttttgga ggggagatgt gg
                                                                 1702
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(2) INFORMATION ON SEQ ID NO. 9:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2067 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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geogragget eceggigite ceatiticgag aggageteet ggetgetatt geaaateace
aagtoctcat cattgaaggo gagacagggt cagggaagac cacccagatc cogcagtatc 120
tctttgagga gggttataca aacaagggta tgaagattgc ctgcacccaa ccccggagag 180
tggctgccat gagtgtggcc gcccgagtgg cccgggagat gggtgtgaag cttgggaatg 240
aggttggcta cagcatccgc tttgaggact gcacatcaga gcgaactgtc ctccgctaca 300
tgacagatgg gatgcttctc cgggagttcc tctctgagcc tgacctggcg agttacagcg 360
tggtgatggt ggatgaggca cacgaaagga ccctacacac agacattctc tttggattga 420
tcaaggatgt tgctcgcttc cgacctgagc tcaaggtcct ggtggcttca gccacaatgg 480
acactgoog titticoacc tictitgatg acgcoodgt gittogaate cooggacgca 540
ggtttcctgt ggacatcttc tacaccaagg ctccagaggc tgactacttg gaagcttgtg 600
tagtatctgt gttgcagatc catgtgaccc agccccctgg ggatatcctg gtgttcctga 660
caggacagga ggagattgag getgeetgtg agatgeteea ggategetge egeegeetgg 720
getecaaaat eegggagete etggtgetge ceatttatge caatetgeee tetgacatge 780
aggcccgtat cttccagccc acaccacctg gggcacgaaa ggtggttgtg gcaacgaaca 840
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cagagetgee ggtggacece atgetgteea aaatgatett ageetetgag aagtacaget1320
gttcagagga gatcctgaca gtggctgcca tgctctctgt caacaactcc atcttctacc1380
gaccaaagga caaggtcgtc catgctgaca atgcccgtgt caacttcttt ctccctggcg1440
gtgaccacct ggttctgcta aatgtttaca cacagtgggc tgagagtggt tactcttccc1500
agtggtgcta tgagaacttt gtacagttca gatcgatgcg ccgagcccgg gatgtgcggg1560
aacagctgga agggctcttg gaacgtgtgg aagttggtct cagttcctgc cagggggact1620
atateegtgt aegeaaggee ateaetgetg gttaetttta ecacaeggea eggttgaete1680
ggagtggcta ccgcacagtg aaacagcagc agacagtett catteatece aacteeteec1740
totttgagca acagccacgc tggctgctct accacgaact tgtcttgacc accaaagagt1800
tcatgagaca ggtactggag attgagagca gttggcttct ggaggtggct ccccattatt1860
ataaggccaa ggagctagaa gatccccatg ctaagaaaat gcccaaaaaa ataggcaaaa1920
cacgagaaga gctagggtaa gagaaggacg taaacagaac ctgacaccag ctccttttcc1980
ttctatacat tatttaatac ctattaaata aaattatttt tggaataaag cttgtgggaa2040
                                                                 2067
catttgggat ctagaaaaaa aaaaaaa
```

(2) INFORMATION ON SEQ ID NO. 12:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2548 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
gccgcagccc tcatctgcca ccgcagtctg gttggagctg ttgtcttgta tgctcagcga
ggcccggaga gacccgggag agagctaggc cgagtccacc gcccgagtct gctgcccgag 120
cocgcgttac gcacaaagcc gccgatcccc ggcctggggt gagcagagcg accaccgccc 180
gggagcagcg cggcgagacg cacggtgcgc cctatgcccc cgcgccccca ccgcccccgc 240
cgcggcagcc gaagcgcagc gagagaacgc gccaccgcgg ggcccgggtg cagctagcga 300
cectetegee acetgegege agecegaggt gageagtgag eggegagegg gagggeageg 360
aggogttege gggccccctc etgetgeceg ggcceggccc teatggegge cateegeaag 420
aagctggtgg tggtgggcga cggcgcgtgt ggcaagacgt gcctgctgat cgtgttcagt 480
aaggacgagt teeecgaggt gtacgtgeec accgtetteg agaactatgt ggeegacatt 540
gaggtggacg gcaagcaggt ggaggtggcg ctgtgggaca cggcgggcca ggaggactac 600
gacccgctgc ggccgctctc ctacccggac accgacgtca ttctcatgtg cttctcggtg 660
gacagecegg actegetgga gaacateece gagaagtggg teecegaggt gaageactte 720
tgtcccaatg tgcccatcat cctggtggcc aacaaaaaag acctgcgcag gacgagcatg 780
tecquadaqa getqqeeeqe atgaaqqaqq aacceqtqeq caeqqatqae qqeeqeqeca 840
tggccgtgcg catccaagcc tacgactacc tcgagtgctc tgccaagacc aaggaaggcg 900
tgcgcgaggt cttcgagacg gccacgcgcg ccgcgctgca gaagcgctac ggctcccaga 960
acggetgeat caactgetge aaggtgetat gagggeegeg eeegtegege etgeeeetge1020
eggcaegget eccetecty gaccagteec eegegageec ggagaagggg agaccegtgt1080
cccacaagga ccccaccggc ctgcctggca tctgtctgct gacgcctctg gcttgcgccal140
ggacttggcg tgggcaccgg gcgccccat cccagtgtct gtgtgcgtcc agctgtgttg1200
cacaggeett ggeteeceae tgagtgeeaa gggteecetg ageatgettt tetgaagage1260
egggeeteag agtgtgtgge tgtgtgtetg ttegaeteee etegeeecat tttcacceca1320
ecceegeete tgateeeegg gggegagatt ggegegggag tgtggeegeg ecceateaga1380
tgttcgccct tcaccagcgg gagettgata tcccttgtct gtaacataga ccccgggtac1440.
tgcgggaggg gagggctgct ggggaggatg gggggatgtt atataaatat agatataatt1500
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```

ggctgggcca gactcccgcc caagcatgaa caggacttga ccatctttcc aacccctggg1620 gaagacattt gcaactgact tggggaggac acagcttcag cacagcctct cctgcgggcc1680 agcccgctgc gaaccctcca ccagctaccg gaggaggag ggaggatgcg ctgtggggtt1740 gtttttgcca taagcqaact ttgtgcctgt cctagaagtg aaaattgttc agtccaagaa1800 actgatgtta titgatitat titaaaggcta aaattigtti tittaticti tgcacaattg1860 tttcattgtt tgacacttaa tgcactcgtc atttgcatac gacagtagca ttctgaccac1920 acttgtacgc tgtaacctca tctacttctg atgtttttaa aaaatgactt ttaacaagga1980 qaqqqaaaaq aaacccacta aattttgctt tgtttccttg aagaatgtgg caacactgtt2040 ttgtgatttt atttgtgcag gtcatgcaca cagttttgat aaagggcagt aacaagtatt2100 ggggcctatt ttttttttt tccacaaggc attctctaaa gctatgtgaa attttctctg2160 cacctotgta cagagaatac acctgocoot gtatatoott ttttcccctc ccctcc2220 cagtggtact totactaaat tgttgtottg ttttttattt tttaaataaa otgacaaatg2280 acaaaatggt gagcttatga tgtttacata aaagttctat aagctgtgta tacagttttt2340 tatgtaaaat attaaaagac tatgatgatg acatttttat aaaagaaatc ttgtggttta2400 atagtgtgta aaaataccct tgtgaatttg gaacaaggga gatattctcc taggcgagat2460 cettlettge caacteegtt teeettatag caaatgtagt aaatgaggat gaagteeett2520 tgagagcatg tgggggttgg gtgaccaa

(2) INFORMATION ON SEQ ID NO. 13:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1673 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

accaatgcac atgtagtaat caaatgtttg gggctagata ttatggtata caaaaaacat taaaatcatg tggtttgcaa gcaaagcaaa catttttgcc aatgtttgca aattggccac 120 aaccacaaat tcaagaaatt ttttaaaaag acaaaagcca gcttacaaag atttgaccaa 180 taaaacccct cgagcccaca gccttatcag ctggggttga gggaagactg gtctaggtgc 240 tgetectgaa ettggtetet gageeatgge tteccataga eacteaggte ecteeageta 300 caaggtggge accatggcgg agaagtttga ctgccactac tgcagggatc ccttgcaggg 360 gaaqaagtat gtgcaaaagg atggccacca ctgctgcctg aaatgctttg acaagttctg 420 tgccaacace tgtgtggaat gccgcaagce catcggtgcg gactccaagg aggtgcacta 480 taagaaccgc ttctggcatg acacctgctt ccgctgtgcc aagtgccttc accccttggc 540 caatgagacc tttgtggcca aggacaacaa gatcctgtgc aacaagtgca ccactcggga 600 ggactccccc aagtgcaagg ggtgcttcaa ggccattgtg gcaggagatc aaaacgtgga 660 gtacaagggg acceptctggc acaaagactg cttcacctgt agtaactgca agcaagtcat 720 cgggactgga agcttcttcc ctaaagggga ggacttctac tgcgtgactt gccatgagac 780 caagtttgcc aagcattgcg tgaagtgcaa caaggccatc acatctggag gaatcactta 840 ccaggateag ecctggeatg ecgattgett tgtgtgtgtt acctgeteta agaagetgge 900 tgggcagcgt ttcaccgctg tggaggacca gtattactgc gtggattgct acaagaactt 960 tgtggccaag aagtgtgctg gatgcaagaa ccccatcact gggtttggta aaggctccag1020 tgtggtggcc tatgaaggac aatcetggca cgactactgc ttccactgca aaaaatgctc1080 cgtgaatctg gccaacaagc gctttgtttt ccaccaggag caagtgtatt gtcccgactg1140 tgccaaaaag ctgtaaactg acaggggctc ctgtcctgta aaatggcatt tgaatctcgt1200 tetttgtgte ettaetttet geectatace atcaataggg gaagagtggt cetteeette1260 tttaaagttc tccttccgtc ttttctccca ttttacagta ttactcaaat aagggcacac1320 agtgatcata ttagcattta gcaaaaagca accetgeage aaagtgaatt tetgteegge1380 tgcaatttaa aaatgaaaac ttaggtagat tgactcttct gcatgtttct catagagcag1440 aaaagtgcta atcatttagc cacttagtga tgtaagcaag aagcatagga gataaaaccc1500 ccactgagat gcctctcatg cctcagctgg gacccaccgt gtagacacac gacatgcaag1560 agttgcageg getgetecaa etcaetgett caeceegttt etgtggagee gggagaaggg1620 accetactgg accatggeat ggggttaact tteeteatea ggaetetgge eet

(2) INFORMATION ON SEQ ID NO. 14:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1593 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
ggggccagga cgccgcccgg cgcggagtgg ctgccctgcg cggggacact cagagcccgg 60
tgggcgggag gaaggcggca tgccccagac ggtgatcctc ccgggccctg cgccctgggg 120
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aggaagcaag gcggcactgc caacctgtgt cctggagatg tcatcctggc tattgacggc 240
tttgggacag agtccatgac tcatgctgat gcgcaggaca ggattaaagc agcagctcac 300
cagctgtgtc tcaaaattga caggggagaa actcacttat ggtctccaca agtatctgaa 360
gatgggaaag cccatccttt caaaatcaac ttagaatcag aaccacagga attcaaaccc 420
attggtaccg cgcacaacag aagggcccag ccttttgttg cagctgcaaa cattgatgac 480
aaaagacagg tagtgagcgc ttcctataac tcgccaattg ggctctattc aactagcaat 540
atacaagatg cgcttcacgg acagetgcgg ggtctcattc ctagctcacc tcaaaacgag 600
cccacageet eggtgeeece egagteggae gtgtacegga tgeteeacga caateggaat 660
gagoccacac agoctogoca gtogggetoc ttoagagtgo tocagggaat ggtggadgat 720
ggototgatg acceptocege teggaacegeg agtetegagag etccegetegac gaaagtocat 780
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tgcaacctca acctcaagca aaagggctac ttcttcatag aaggggagct gtactgcgaa 960
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gtcaaggett tagacettta teetattgtt tattgaggaa aaggaatggg aggcaaatge1200
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cagocatcaa acacataaac atcaagatat ttgaaggact ctaattgtct ttccttgaca1380
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agttgtctgt atgtgtttta actattacag tgcatgttag ggagaaattc cctgaatttc1500
tttagttttg tattcaaaca attatgccac tcgatgcaac aaacataata aatacataaa1560
agatttaaaa aataaaaaaa aaaaaaaaa aaa
                                                                 1593
```

(2) INFORMATION ON SEQ ID NO. 17:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1722 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```
cattgtttgc caaaatccca ggcagcatgg acctcagtct tctctqqqta cttctqcccc
tagtcaccat ggcctggggc cagtatggcg attatggata cccataccag cagtatcatg 120
actacagcga tgatgggtgg gtgaatttga accggcaagg cttcagctac cagtgtcccc 180
aggggcaggt gatagtggcc gtgaggagca tcttcagcaa gaaggaaggt tctgacagac 240
aatggaacta cgcctgcatg cccacaccac agagcctcgg ggaacccacg gagtgctggt 300
gggaggagat caacagggct ggcatggaat ggtaccagac gtgctccaac aatgggctgg 360
tggcaggatt ccagagccgc tacttcgagt cagtgctgga tcgggagtgg cagttttact 420
gttgtcgcta cagcaagagg tgcccatatt cctgctggct aacaacagaa tatccaggtc 480
actatggtga ggaaatggac atgatttcct acaattatga ttactatatc cgaggagcaa 540
caaccacttt ctctgcagtg gaaagggatc gccagtggaa gttcataatg tgccggatga 600
ctgaatacga ctgtgaattt gcaaatgttt agatttgcca cataccaaat ctgggtgaaa 660
ggaaaggggc cggggacagg agggtgtcca catatgttaa catcagttgg atctcctata 720
gaagtttetg etgetetett teetteteee tgagetggta actgeaatge caactteetg 780
ggcctttctg actagtatca cacttctaat aaaatccaca attaaaccat gtttctcact 840
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tatacagtgc gcatgcttac agccgggctt ctggagcacc agctgcagcc tggctactgc 960
tttttactgc agaatgaact gcaagttcag catagtggag gggagaggca gaactggagg1020
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caaaagcagg ctttctgccc tgagggacat cttcccactc ccctgctcca catgagccat1140
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aaatggggaa atggaagggt ttggaggcag agctgaaaac agggttggaa ggatttcctg1260
aattagaaga caaacgttag catacccagt aaggaaaatg agtgcagggg ccaggggaac1320
ccgtgaggat cactctcaaa tgagattaaa aacaaggaag cagagaatgg tcagagaatg1380
ggattcagat tgggaacttg tggggatgag agtgaccagg ttgaactggg aagtggaaaa1440
aggagtttga gtcactggca cctagaagcc tgcccacgat tcctaggaag gctggcagac1500
accetggaac cetggggage tactggcaaa eteteetgga ttgggcetga ttttttttggt1560
gggaaagget geeetgggga teaactttee ttetgtgtgt ggeteaggag ttettetgea1620
gagatggege tatettteet eeteetgtga tgteetgete eeaaccattt gtactettea1680
ttacaaaaga aataaaaata ttaacgttca ctatgctgaa aa
```

(2) INFORMATION ON SEQ ID NO. 18:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1648 base pairs
 - (B) TYPE: Nucleic acid(C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- ((xi)) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
tgaccaagaa acagggccta aggatcattt tctcggatgc atcacggctc atcttccggc
teagtteete cagtggtgtg egggeeacce tgcagaetgt acgeagagag etacgagagg 120
gatoccagog gocatgacca ggagocacag gcagtgotga gccototoat agocatogca 180
ctgaaaatat cccagattca tgagagaact ggccggaggg gacccactgt catcacctga 240
atagaggaaa gatcactcac cagggccaaa gagagtgctc agcgggagat gcttcactga 300
tgccttcttg ctacctgttt gtgcctctta tgactttgga aaaacaaaag atattttgct 360
tttgggggat agagggtggg tgggaaaaga aaaaaaatcc atttggtttt ggttttgtcc 420
tatteeteea aatgeageag ggeetttagt tgtetgttaa agetgeacta taatttggta 480
tctacatttt atcacacaaa ggaacctccc cttttgacaa caactgggct aggcagctgt 540
taatcacaac atttgtgcat cacttgtgcc aagtgagaaa atgttctaaa atcacaagag 600
agaacagtgc cagaatgaaa ctgaccctaa gtcccaggtg cccctgggca ggcagaagga 660
gacactecea geatggagga gggtttatet ttteateeta ggteaggtet acaatggggg 720
aaggttttat tatagaacte ecaacageee aceteactee tgecacceae eegatggeee 780
tgcctccccc atcccatccc caacatccct gtaccacctt ctctcacatc ttctaaagct 840
ttgtacaaat cacaatggtg cacttccaac aaaatatatc aataggtgtt ttcctctctt 900
attttgtaaa tagtattatt ttagctatta agctggatac cttctttcaa attcagccat 960
tcagttgtaa agttgggaag aagtttcttg acaagactct gcaattaaat gcttaaaatt1020
tggaggggat ccttccttga ttacatcaag tatgttggta catgggttta tacaagttcc1080
tettgagaag geaaaaagae caccatgtgt gagagetett tgaettggee aataggggee1140
tatcttaatg cacttgtttg gacacatttc tgatcttatt tgtaaaggct gcaaaaggag1200
aggatgaaat gctgtaaaag taggaaatga agtggaagct ggaagaaaat gtaattggtg1260
gtacagetat gggccagatg gtggagggga gggtggggae ceetgeegge aagcagagtg1320
teacagetgg ettteeteae ttgggaaaag ggtaetgeeg gtetageage etectetgta1380
ctcagccagg acacccagcg cgtgggacct gtttgtgtct gttttgcttc cttgggaacg1440
gcacagtcac tcaccctgcc atttgcggaa atgacctggt gcactttgac tgttaagcaa1500
tgcgttattg ctgtagtcaa ggttagtgca agcaaggaaa cattcccagt aaggtatttg1560
tttccatttt ctgtctgtgc ttctgtcaga aacttgctag gactttagtg gccaataaaa1620
```

(2) INFORMATION ON SEQ ID NO. 20:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1610 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

gegegetgat tggaegegtg gggegaggeg gaggagagee gtgegeaegg egtatgtggg geogtgtgca gaccogogtg tggogcaggc aaggaccotc aaaataaaca goototacot 120 tgcgagccgt cttccccagg cctgcgtccg agtctccgcc gctgcgggcc cgctccgacg 180 eggaagatet gaetgeagee atgageagea atgagtgett caagtgtgga egatetggee 240 actgggcccg ggaatgtcct actggtggag gccgtggtcg tggaatgaga agccgtggca 300 gaggtttcca gtttgtttcc tcgtctcttc cagatatttg ttatcgctgt ggtgagtctg 360 gtcatcttgc caaggattgt gatcttcagg aggatgcctg ctataactgc ggtagaggtg 420 gccacattgc caaggactgc aaggagccca agagagagcg agagcaatgc tgctacaact 480 gtggcaaacc aggccatctg gctcgtgact gcgaccatgc agatgagcag aaatgctatt 540 cttgtggaga attcggacac attcaaaaag actgcaccaa agtgaagtgc tataggtgtg 600 gtgaaactgg tcatgtagcc atcaactgca gcaagacaag tgaagtcaac tgttaccgct 660 gtggcgagtc agggcacctt gcacgggaat gcacaattga ggctacagcc taattatttt 720 cettegece coetcettet tetgattgat ggttgtatta tettetetga atectettea 780 ctggccaaag gttggcagat agaggcaact cccaggccag tgagctttac ttgccgtgta 840 aaaggaggaa aggggtggaa aaaaaccgac tttctgcatt taactacaaa aaaagtttat 900 gtttagtttg gtagaggtgt tatgtataat gctttgttaa agaaccccct ttccgtgcca 960 ctggtgaata gggattgatg aatgggaaga gttgagtcag accagtaagc ccgtcctggg1020 ttccttgaac atgttcccat gtaggaggta aaaccaattc tggaagtgtc tatgaacttc1080 cataaataac tttaatttta gtataatgat ggtcttggat tgtctgacct cagtagctat1140 taaataacat caagtaacat ctgtatcagg ccctacatag aacatacagt tgagtgggag1200 taaacaaaaa gataaacatg cgtgttaatg gctgttcgag agaaatcgga ataaaagcct1260 aaacaggaac aacttcatca cagtgttgat gttggacaca tagatggtga tggcaaaggt1320 ttagaacaca ttattttcaa agactaaatc taaaacccag agtaaacatc aatgctcaga1380 gttagcataa tttggagcta ttcaggaatt gcagagaaat gcattttcac agaaatcaag1440 atgttatttt tgtatactat atcacttaga caactgtgtt tcatttgctg taatcagttt1500 ttaaaagtca gatggaaaga gcaactgaag tcctagaaaa tagaaatgta attttaaact1560

(2) INFORMATION ON SEQ ID NO. 21:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1108 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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qqaqqqqqq gqaqaqtagq gtqctqtqqt ctqaqctaqa qqqtqaaqct gqcqqacaqq 60
aggatgggcg tatgcaggtg atagactaga gaacaagacc tctgtctccg tagcatcctg 120
ggcgagcagt ctgaatgcca gaatggataa ccgttttgct acagcatttg taattgcttg 180
tgtgcttagc ctcatttcca ccatctacat ggcagcctcc attggcacag acttctggta 240
tgaatatega agtecagtte aagaaaatte eagtgatttg aataaaagea tetgggatga 300
attcattagt gatgaggcag atgaaaagac ttataatgat gcactttttc gatacaatgg 340
cacagtggga ttgtggagac ggtgtatcac catacccaaa aacatgcatt ggtatagccc 420
accagaaagg acagagtcat ttgatgtggt cacaaaatgt gtgagtttca cactaactga 480
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gacctatett tggcgttgce agtteetttt acettttgtg agtttaggtt tgatgtgett 600
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```

(2) INFORMATION ON SEQ ID NO. 22:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

agggaaagag agaagaggc ctagacgaac acaatcacat gttttctttg ctgttcctcc 60 cgggatggc ctgttttggg gtttgggact ctgaacccga gcggggttcc ttcgcttgac120 tttgatcctg gtccttaaat gcctttcccc actcccctcc cgtgggttca ggggccaagc180 ggcccctcct cagagcacgg gcagcaccgt ctcctggacc cctgtgtgcc agcctctgca240 gacgcagctg gtgggagga gcatggattt ggaggtggag aagtcactcc tggtcctcgg300 agggggtggg ctgtgtgcct agttcagtgt gactcgggaa ttggtgaggg cggacaggtt360 tctgaggcct ccctagcctt ctttgtaaat tcacacgaga tagtccaggg ctttccagcg420 cccagcttgg atgataatcc tcgtgtcccc cactctaagg cctccttgag attttttgg480 ggtctaccac gtcctctgcc tgtctccagg tggtacagga gatgtggtc ctgtccctct540 cctgggtccc tagggggcc cagggcccct ccctgtagc ttagctgacc ccatggtgt600 gggtgtgggg gggag cccaggta agcttgggg ctccaggta gcggtcccga660 agaacggggg gggag

- (2) INFORMATION ON SEQ ID NO. 23:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

agcagagcaa ggttgggttc gctcctctgg cagaacctcg gctctcagga ggtccttgtt 60 ccagggaaca gctgcttctc tgggggctgg ggcttctaac ttccctggca gcccctcggc120 actaacccag ctggaaacca ggggaacaaa cggcctggag tgccaaaccc ttcgtgtcta180 tttttccag aaaaacgggg gcaatggctg ttgaggagcc catttgggaa gaactggtgc240

ctctaatggg gcaaatggat tctgcagggg gctgcagttg ggcagggaaa attccttcaa300 acaaggggtt ccacccaaac ccaggccccg gcttcaaatg gccagaaaaa 350

(2) INFORMATION ON SEQ ID NO. 24:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 746 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

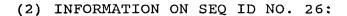
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

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(2) INFORMATION ON SEQ ID NO. 25:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 217 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

agtgtatggc agcaaatgag ggatcataac totcagttta ttgatgatta ttcatootca 60 gatggaggag tttatoogtc agccacttca gtttogtott aaaacaggag cocacaggac120 ccaaggaact attaaggagg accaggaacc taggttttt otttcaaaaa attggcoota180 gcccaataaa tgaaggaaaa aattaggcac otttttt



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 392 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

geggateegg egtteteeae tgatetttte caaggetgta cagacatgge ggeggetttt 60 cggaaggcgg ctaagtcccg gcagcgggaa cacagagagc gaagcagtga ctaccgtaaa120 aaacaagaat acctcaaagc tcttcggaag aaggctcttg aaaaaaatcc agatgaattc180 tactacaaaa tgactcgggt taaactccag ggtggagtac atattattaa ggagactaag240 gaagaagtaa ccccagaaca actaaagctg atgagaactt caggacgtca aatatatagg300 aagggaagag ggtgcagaag ctaagaaaat cgaagactaa aatcagggcc catctgcggg360 ttgcagggga ggcaggaaaa ggttgttttt tt

- (2) INFORMATION ON SEQ ID NO. 27:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1796 base pairs
 - (B) TYPE: Nucleic acid (C) STRAND: individual

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

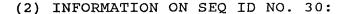
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(2) INFORMATION ON SEQ ID NO. 29:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2927 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

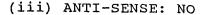
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- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 743 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

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- (2) INFORMATION ON SEQ ID NO. 31:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1667 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO



(vi) ORIGIN:

(A) ORGANISM: HUMAN

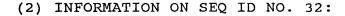
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

agagccaata gcatggggtt tacaaggcaa agatagtcat tcattcaaca catattcata gageteette tetgtgeeag acaetgttet ggaagatage tagatgaaaa tetttgeact 120 cacagagett acatgccagt gagtgaagat egatgataaa taaagcaaat gcatcatatg 180 ttcacatttg ataagtatat gccaaaaaat gaagccggga aggaggacaa ggcccatggg 240 tggqtgttga ggtttttaaa gtgtggtcag gaaaggcccc actgataagg taacatttga 300 gcaagtctga aaaaggcaag gggatctttg gggctaactt cgggatccct gcactttatg 360 taagaatgta aacctggagt ctcatttaag aatgatcagc aatacgttta gaacatatga 420 actgaatgaa atggacattt tttcttaatt tacgtataaa tccatatgat tatacataaa 480 gttctgatgc attaataaaa gcagccaaat agggccaaag agaaaaataa caggactctg 540 tactggacct aactttatca ttaattaggt aatattttcc tcatttcttt actgctgcca 600 ttttcctcac cagtattcca gagatggtca tagctcatta ctctaccacc aagaacctaa 650 aaggaattag aatacagcag aattggcctc agtgaagagc ttaaaattgt tctcctcgta 720 gaactggact attgatcatt accacgtgac gttggctcta ttactttctg ttcccaatgt 780 ccttctagtg gtttgaaaat gttaaaacat ccctaaaatc taaatcatat aatcagaatt 840 ctatagtgtc ccactctatc tgtaaagatc atttggaaga ctttagactc tattaatttt 900 aaaaggaata tttattagcc atatgcagaa tttctaatga tgatattgta cagcttctaa 960 ttcacttttc agatcagtgt ttgaaatggc aattatcagt gttggattta gttccaacta1020 cttgatttac aaaaatgtac atttagagaa ggttaaaaga aacagtgaga aatgtaaaca1080 ttcaaaatga taattgaatc tctcagttgt gggaataatt atcagagaca tgcaactgaal140 aatgtctcac cttfcatctt tttttcttaa ttcataaagt tatcttgtag aatttgatga1200 gaccetecta gteattetea actggggegg tgetgteace gaatggtgtt tgagagtgtt1260 ggggctaggg cacatttttg gttgtcacag caactggggt ggcatttgct gcccagtgcc1320 aggaatagta acattatgaa tgccagggac agtgtgctca gtaaagtctt ccatccaaaa1380 ggggcagggc acgggtgctc acgcctgtaa tcccagcact ttgggaggcc aaggtgggcg1440 gatcacctga tgtcaggggt tcgagaccag cctggccaac atggtgaaac cctgttgcta1500 ctaaaaatac aaaaattggc tgggtgtggt gtcacatgcc agtaacccca gctactaggg1560 aggetgagge aggagaatea ettgaaceeg ggaggeagag gttgeagtga getgagattg1620 caccactaca ctccagcctg gatgacagag tgagacttca tctcaaa



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

cgtggtaggc acttcatcag tgtttactga ttgaaaacat tgttgactgt ggcttctatc 60 agagtgtcta ccttttacag ctctgaccct acctcattta atttgctgct tttaatctac120 gggggctgag aatttgtgaa accagtgttg ttagaagtgt atataatctg aatcaataag180 ctctgaatgg gggacaagaa acgctcttat agcacaaaga tgcatggact tcatgacagc240 tcttttggt

- (2) INFORMATION ON SEQ ID NO. 33:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1246 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

aatggaaggt taattaccgg ggcccacctt gagacggaaa aaaattggga aaacgaaact aaaaatggtt ggggtgaatt tctacccaaa gtccagccgt ggtggctgca ctggcacaga 120 atactaaact gagtgtgact attttcaatg caacaaatga aaaaacaaaa tgtgcctgtt 180 taaagcactc agtagagggc tgatgaaact aatttttttt cctttaagac atgcactctt 240 gagtectaca gtaactgagt gtttgtttag acagcacaag aaggggtgag agtgegtete 300 ctaqccttaa tgtgggaggg tagtttcagt cactcatcgg ctttcattat tgtgcagaaa 360 tattagaaaa cctcattgat caattttatg tatttgaata tcagcaaatt gaaattttcc 420 ataattatca ttaatttgta accacatcca gtgtcatgct tactccttag agttcagatg 480 aattottaaa attaaaaaaa aactocatag tactaatttt gtttotttat atagtttgcg 540 tttgatatta gtgcttgcaa ttgtattaaa gtcaaaagct gatttttatg gcatacacaa 600 gaatgccact ttttctttta tttcatacca ataatttaaa gattgatatg ctaaaaacaa 660 tttgcacage actaaageat gagetaettt catetaaace tgtaaaaata tgaaagattt 720 ttatattttt tcactgggaa gaaattcttc ctggatgaaa ttacaaatat gtgtagaata 780 tatttaataa aagacttata aaatacctaa ctacaggact taaaatatag attggcgcgt 840 agtatataga acaatattcc atataaataa gtttagcctt tataaaaatg aagttgcagg 900 ctgacattac attctgtact tactaagtgt caacagccct tacaaacatt aaatgtaaat 960 ggtttcaaat ggtcagcgtt gtttaaatgt aatcatgtta ttttattcat tgttaatgct1020 ttgatgaaaa ggctttatat gcagtagatc tacgaaaata ttgttcatac tgatcagaat1080 taaatttgta tagagcagag ttttaaaatg aatgtaaata gcactaaacg ttttctttct1140 gcaacctgta cttacagatt cttcctgtaa actaaataaa aaaaaaatga tagtgcaaaa1200 1246 aaaaaaaaa aaaaaaagag acggagagag gagaaagagg gcgtgg

- (2) INFORMATION ON SEQ ID NO. 34:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 215 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

gggaagcatt ttggatatga tgcaggaaat ctcttcctgg agtcaaaagt tcccaagagg 60 tgctgtattt ttaagaaatg gagtttattt aaataatagt taagcttgtg cccatgttgg120 ccgggcaact tttttcaatg gtgcttatta gaagaagtgt tttcatctgg tcaatttaag180 gaaataaaac taggaaatgg agagggggg agaga 215

(2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 734 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

getgeeggg geetggget eggegteggt eeeeggggga tgtggaage tggeageatg 60 teggeeggg tggagtegg gtgeegettg eggeeggtga aegagegegt geageaget120 gtggegegge ggeegegga teteceagee atecageee ggetagtgge ggteageaaa180 aceaaacetg cagacatggt gategagge tatggacatg ggeagegeae ttttggegag240 aactacgtte agaaacagea teaaateeea aaattetgte tttgtgteet300 gagateaaat ggeactteat tggecaceta cagaaacaaa atgteaacaa attgatgget360 gteeceaate tetteatget ggaaacagtg gattetgtga agttggeaga caaagtgaac420 agtteetgge agagaaaagg tteteetgaa aggttaaagg ttatggteea gattaacace480 ageggagaag agagtaaaca tggeetteea eetteagaga eeatageea egtggageae aaateetga gtggggetga tgaceatagg aagetttggg600 catgatetta gteaaggae aaateeagee teetgagtta aaagetgaae acegggagaag getgateaa ateeetgetg tattgteget eeeggaagag660 actgtggtaa aaagetgaae ateeetgetg aacaggttga getgateatg ggeatgteeg720 tetgtaaact geaa

(2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

getgetgggg agceactgaa ccaaccggag accegetggt cccacgtgaa gcagctgtcc 60 tggtgtggag gtacagagct agaccagcac tggtccetcc agceccctgg tagectctgc120 tgcaactgaa ctggcagctt ttgccgctgc ctttagetct gcatgtatgc gccctgaagg180 ttctgcctct ctgttttgga atcgccttcc cctcctcatg tttggggacc tgcaagggtg240 tgagggcacgt gagggcatcg ccatgcgtat tttacaggcc tctttctctg gactgtcttc300 aaagggatga cttt

- (2) INFORMATION ON SEQ ID NO. 37:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1839 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

gcgggcgagg gcggagcaac agagcggccg ggagtaaggc ggagtgagag gaggagcttg atggaagcgt gcgagaaggg gcgtaactga tttggaaacc agaggaaagg cgctgttttc 120 accgaattag aatcgcggga aaatagagaa gagtttgttt gaaggtctcg cgagatcgag 180 tgagtacggc tcgccaagtt ggagcgctct cgcgatagac acagcaacta ttcagctgcg 240 aggggacggg agaggtggtg agcactcteg cgagatttga aggageggeg gaggecagag 300 ggaggagagg accggaagte etteatetea ageateeaat getgaaaegg geetgatttt 360 ctctaccgga agcccttttc cagaggctgg gaacacggcc cacctagcag gaagtcccac 420 ctecttgage teegecacee tteeegaagt tttteetgtea cetgtgttag geteegteee 480 ettteegegt tttateeceg taccagaaaa ggatacattt agtgeeteee acceagetee 540. actaaacggc cttcccgctt cctgtggttg tggccgctgt gctgtgggga gcggccccga 600 ecoggggget cattegageg aceteggace acaatgecag catggacttt geagacette 660 cagetetgtt tggggetace ttgagecagg agggeeteea ggggtteett gtggaggete 720 acccagacaa tgcctgcagc cccattgccc caccaccccc agccccggtc aatgggtcag 780 tetttattge getgettega agattegaet geaactttga ceteaaggte etaaatgeee 840 agaaggetgg atatggtgee getgtagtae acaatgtgaa tteeaatgaa ettetgaaca 900 tggtgtggaa tagtgaggaa atccagcagc agatctggat cccgtctgta tttattgggg 960 agagaagete egagtaeetg egtgeeetet ttgtetaega gaaggggget egggtgette1020 tggttccaga caatacette ecettggget attaceteat ecetttcaca gggattgtgg1080 gactgctggt tttggccatg ggagcagtaa tgatagctcg ttgtatccag caccggaaac1140 ggctccagcg gaatcgactt accaaagagc aactgaaaca gattcctaca catgactatc1200 agaagggaga ccagtatgat gtctgtgcca tttgcctgga tgaatatgag gatggggaca1260 agetgegggt acteceetgt geteatgeet accaeageeg etgegtggae ecetggetea1320 ctcagacccg gaagacctgc cccatttgca agcagcctgt tcatcggggt cctggggacg1380 aaqaccaaqa ggaaqaaact caaqggcaaq agqagggtga tgaaggggag ccaagggacc1440 accetgeete agaaaggace ceaettttgg gttetageee eaetetteee accteetttg1500 gttccttage eccagetece ettgttttte etgggeette aacagatece ccactgtccc1560 etecetette ecetgttate etggtetaat aaccecccac acatacacet etggtgacet1620 attrgcacag acceptestet tecetecagt ettetgaggg ataggggaca ttecatecca1680 agetteteee ttacccacae ctateetttt gaggggettt ggggtgggge tggggcaage1740 agagggactg ggtcttcact tcttgggcta ataaaattgt ttctttgtgg actaaaaaaa1800

(2) INFORMATION ON SEQ ID NO. 38:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1931 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

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cagoogoogo coatoootot ttgtgtgott tggaaagoog oggagotggt ggtggotaca 60
gttggtgttg ggggcttagg cgagggacgt taccgggaag ttgcaggcgg gaggactctt 120
coccatocag toacotgaca ggtoacaaac atgtoagaca aaagtgaatt aaaggotgag 180
ttgqaacqta aqaaqcaqcq actqqcccaa atcaqaqqqq aaaaqaagaq aaaaqaagaa 240
qaaaqqaaaa aaaaaqaaac aqaccaqaaq aaqqaaqctq ttqctcctqt qcaaqaaqaa 300
tcaqatcttq aaaaaaaaq gagagaaqct gaaqcattqc ttcaaaqcat ggggctaact 360
ccagaatccc ccattgtccc tectectatg tetecatect ecaaatctgt gageactcca 420
agtgaagetg gaagecaaga etetggagat ggegeegtgg gatetagaeg aggaeetatt 480
aaacttggaa tggctaaaat cacgcaagtc gactttcctc ctcgagaaat tgtcacgtat 540
acaaaggaaa ctcagactcc agttatggct caacccaaag aagatgaaga ggaagatgat 600
gatgtagtgg ctcctaaacc acctattgaa cctgaagaag agaaaacttt aaagaaagat 660
gaggaaaatg atagtaaagc tcccctcat gagctgactg aagaagaaaa gcaacaaatc 720
ttgcactctg aggaattttt aagtttcttt gaccattcta caagaattgt agaaagagct 780
ctttctgagc agattaacat cttctttgac tatagtggga gagatttgga agacaaagaa 840
ggagagattc aagcaggtgc taaactgtca ttaaatcgac aattttttga cgaacgttgg 900
tcaaagcatc gggtggttag ttgtttggat tggtcatctc agtatccgga gttactcgtg 960
getteetata acaacaatga agatgeeect catgageetg atggtgtgge cettgtatgg1020
aatatgaaat acaaaaaac taccccagag tatgtgtttc actgccagtc agctgtgatg1080
totgccacat ttgcaaaatt toatocaaat ottgttgttg gtggtacata ttcaggccaa1140
attgtgcttt gggataaccg tagcaataaa agaactccag tgcaaagaac tccactgtca1200
gcagctgcac acacacaccc tgtatattgt gtaaatgttg ttggaacaca aaatgctcac1260
aatotqatta goatototao tgatggaaaa atttgttoat ggagtotgga catgotttoc1320
catccacagg atagcatgga gttggttcat aaacagtcaa aagcagtagc tgtgacatct1380
atgtccttcc ctgttggaga tgtcaacaac tttgttgttg ggagtgaaga aggttctgtg1440
tacacagcat gccgccatgg cagcaaagct ggaatcagtg agatgtttga ggggcatcaa1500
ggaccaatca ctggcatcca ttgtcatgca gctgttggag cagtagactt ctcacatctt1560
tttgtcactt catcgtttga ctggacagta aagctttgga caactaagaa taacaagcct1620
ttgtattcat ttgaagataa tgcagactat gtttatgatg ttatgtggtc acctacccac1680
ccagccctgt ttgcctgtgt ggatggcatg ggqagattgg atttgtggaa tctcaataat1740
gacacagagg taccaactgc cagcatttct gtggagggta atcctgctct taatcgtgtg1800
agatggaccc attctggaag gggaggtggt tgttggcggga ttctgaagga caagttttgt1860
tattttgcga tgttgggagg agcagtttgt tggtcccccc aatgatggat tggcgacggt1920
tggcccgacc c
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- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

agttaccatt gccttttctg tctcgtgccg gttttggttt gctgaaacta gtccaaaaca 60 ggaaatttaa cagacagcca cagccaaaga gtgtcatgtg aattacaaga aatagagccc120 atttagggaa agatagaact agaaaggctt ttcattataa ttccatgttg aacaattgag180 tcatagcttc ttatcttgga ggaaggacac aattcaaagg ggcagtaagg attttgtaaa240 acgtggcatc cataatttac tatggagcaa gtgcccacat ctctaggaca ttaa 294

- (2) INFORMATION ON SEQ ID NO. 40:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 882 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (5) 101020011 11...001
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ttttttttc tcattaacaa agcagtcaat tccctttatt tttaaaattt tatgtacaca 60 tatgaatgat ctgtataatg tacattcaat atagaaagct ttatatattt gatagtgtat120 agaacatttc acaaattacac tcatcttta cataacatct tgacatccat ttttaaattt180 ttttgcacaa gctccttttc attcaatttg gtaaagccag ttatacatac taatgtgtac240 tgtgagcttt cagaaggtta atgattgagg atgccagtga agggtgcagg gacaaaacct300 aatagtcttg gatggtgggg ggaggatggc cacgcagact tgatgcagga gagggaaata360 ttcttcctg gggaaaagtg acttagcca atttttgttg actgtagctc aaccctacag420 tcatgctagt tcaaaaaaaa aattacaaaa actaggaaga aagttttgt ttttttgattc480 acagttttgt aaacagatat aaaggaacaa atgtgcttac atacaccaag aaaaaaaaa540 ttcttgtgta cccacttatg ttgatccaca gagtgctttc ttataatgtg atacaattag600 gatcactgac tttttttcct aaaaaatatat ttatagaaaa aggaataaca ctggtgagat gtggacttgg720 cactggcctt tcagcgttta ttgtctctcg tgaatattc aaggtcgaa ggcaaggtcg780 cctgcctcat ggtctacaag aggtggcagg ttagacatga ctgatgtaga tgtactgcg840 taaggtagcc agcaactcca ggtcctgctt cagagagcta ca 882

- (2) INFORMATION ON SEQ ID NO. 43:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 934 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ctcqcqccqq acacagggag caqcqaqcac qcqtttcccq caacccgata ccatcggaca 60 ggatttetee geeteageee aacggggagg getagttgea catagtgatt tagatgaaag120 agctattgaa gctttaaaag aattcaatga agacggtgca ttggcagttc ttcaacagtt180 taaagacagt gatetetete atgtteagaa caaaagtgee tttttatgtg gagteatgaa240 gacttacagg cagagagaaa aacaagggac caaagtagca gattctagta aaggaccaga300 tgaggcaaaa attaaggcac tcttggaaaq aacaggctac acacttgatg tgaccactqq360 acagaggaag tatggaggac cacctccaga ttccqtttat tcaggtcagc agccttctqt420 tggcactgag atatttgtgg gaaagatccc aagagatcta tttgaggatg aacttgttcc480 attatttgag aaagctggac ctatatggga tcttcgtcta atgatggatc cactcactgg540 totcaataga ggttatgogt ttgtcacttt ttgtacaaaa gaagcagctc aggaggctqt600 taaactgtat aataatcatg aaattcgttc tggaaaacat attggtgtct gcatctcagt660 tgccaacaat aggctttttg tgggctctat tcctaagagt aaaaccaagg aacagattct720 tgaagaattt agcaaagtaa cagagggtct tacagacgtc attttatacc accaaccgga780 tgacaagaaa aaaaacagag gcttttgctt tcttgaatat gaagatcaca aaacagctgc840 ccaggcaagg cgtaggttaa ttgagtggta aagtcaaggt ctggggggaa tgttggaact900 gtttgaattg ggggtgttcc gcttaggaag gttc

- (2) INFORMATION ON SEQ ID NO. 44:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ctcgtgccgg tcaattatga gttcctttat ttattggtga gaaagattag caagtatgac 60 gtatgcaagg aatagaagtt atgtaccgag tggttaaagg ttggggggat atggagatgg120 atgagaggga gctgtctggg aaggctttgc ttcacttgga ttagagtagg gttgcgtgag180 gaaataggtg tgtagaatga gaatgagggt catgacagcc tcctacaaaa c 231

(2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

cgatcacgtt ttcacatgat gctcacgctc agggcgcttc aattatccct ccccacaaag 60 ataggtggcg cgtgtttcag ggtctctcgt ctctccta cagaaaagaa aaagaaaaaa120 atgtcattag aagaggcgta acacgtcagt ccgtccccag gtttgtgttt cctggagtgg180 ccgaaagaga tcagttctaa cctgctctgc aggaataacg gtcctqcctc ccgacactct240

- (2) INFORMATION ON SEQ ID NO. 47:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

agagcagatc agaggcaggg ggaaaagcac gcagagggag gagctgaaga gctgagaccc 60 ggagccaggg acagcttaat gaagacaaac tgaaggggaa actgagatgc ttagaaagcc120 cagctataca actctaccca gaaatacttc ccttagggaa tgtaaaaagt actactggag180 atggaagagc agaaaaacag ctatgggcag aaggccaagg ggtgatag 228

(2) INFORMATION ON SEQ ID NO. 48:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1229 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

aaaaaaaaaa aaaaaagagt taatctagga gataatgaat ggcctagtac tagataatat 60 atggccccac aagctettga ettetgteet tggggaaage cattttgtta accacactag 120 tgagatttac atgatgctta atggagaaca gagaagatct tgttgcaaaa ggtgtattaa 180 atatttgtgc tgtttctgta tgagattgag aagcttttcc cacctctcac ccctatttcc 240 tataaggata tocagagaag ocaaactgtt ctgtgggttt gggaatggto atttoccggg 300 aaaatgcatc tggatcgatg actaaacctg gcccttttct ctgggctgta gtgaagccgc 360 attiticacgo tggctggcag tgtgctgaga gcctcgaatg ctctgcggcg tagtgccctt 420ctgccctgcc tgacgatgta tcgaaaagat gagagtgaag gagactttgt gcagcaggaa 480 acgggtaggt gaggtgttgg gcagttgtgg gaacttctga gagtattaca gagtggtaga 540 atèggtaaga actotgatti ggacticgot tiggtggaac tgtgtgccta tacotgcctg 600 tgtgtgtgca agtgtgcagg ttcctttgta tgtatgtgta cgtgtgggaa cctgtgtttg 660 tcatattttt cttcatttca caaaggettt ttttgaagca gtggcagtat geetttgttt 720 caagaacaca tgaaattctt ttaacaccag attagtgtgt taccccaaat gaacggttct 780 agccctctat taagaaataa agggaccata agcattttgg ctgcttatgg ctgtgtgtta 840 ctacttacaa gagtcttgaa aattatacag aactttgcct tcttttttta atgtcttcca 900 caatgttgtg actgattata accetgttte ceetcagaga agagetatgg etcagggate 960 tgtgttgact ctggcattta gtggctttgt gaaggaaaga aaccattaaa tgacctgaca1020 aaaactgact catgtcttta aagtagttga agccactttt aggaatgtta ctctcggttg1080 cttttgtcta attctaatgg gcttaaagcc aagaaaacca tagtataaat cttttttgtg1140 taccctatgg ctagtgtttt aaatgggcag ttccgttgtg gataaagtat ccagtcactt1200 caggtttccg tggaaggttt ttattgggg

- (2) INFORMATION ON SEQ ID NO. 50:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

gaggeeggga gtggaacece etettttgag aaggttgeet gaeteagaga cacagaaaeg 60 ggteeaggga tggggagaga tgtggagtga gggaaggttt geatttgaga aaggaagtte120 gagaacacae tgggacattg taacacattt gaaceatett etgatagaaa ggtgttggee180 teetaataat gggaggteag ggeeaggtee tegggeatag ggagagggte e 231

(2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1340 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
tttggcatca tttacaattt catagaatta ctgtgaaggc ctttctagtt gagatgttgg
ggtatttggg attctaattg ttaaccccag aagaaggtaa tttagcttgt atttatttaa 120
aacccattta gootttact tatatotggt agaattocag tgatcatoot aataaggtat 180
atttcagaat aattttttt toottcagaa taacttagaa toagatgota taagggotoo 240
taggagcagt gtgaaatttc cgtaaagata aatttgaatg ttgtaaccaa gtttatatta 300
aaccaagagg ccatttccaa tatgattttt tgtttctttt taacttgtta agtccctaag 360
agattacatg ctagggcttg agtcatttct attgtagata atgatggccc acacagtcac 420
cttcaactat ccacataagc taggetttee gettttgeea eggacagtgt gaccaagata 480
tttccagagt aaataaccca ccacaacctt ggtaattcct cttttcttct taagctccag 540
gaagegaaag cagaaggaet etttteagae tgeeetetgt ageetaeatt geagetttee 600
aaaacaggca gctagcactg ggaaagccca tgtggtgacc ccatattttt ctgaggttct 660
tottttccat ggtgttactt tattatcaga aagtaaattc agaaaacagg tottgccctt 720
agcagacaag aaccacacca gtttcttgta aaggtaacgg atacattggg attcaggagt 780
gacacagagg tecageeeca gaacttgtaa ggattttgtt tgaacactga geagatgeet 840
cctccctgcc acccatcaca ctagttaggg ctggccatga attctatgcc agagtcactc 900
ttgccttcac agagtcctcc ttgacacccc tgacttaatg atagttgctg ttttggagta1020
gaattgatca ggtttaagtc atcctgctca ggttgggcat agtggctcat gcctgtaatc1080
tcagcacttt gggaagccaa agtgggagga ttgcttgagc ccaggagttc caaaccatcc1140
tgggcaacag agggagaccc tgtctctacc aagaaaaaaa aaaaaaaaa aaagttaaaa1200
aaacaattag ctggacctgg tggtgcacac tcagtaggct gaggtgaaag gattccttta1260
acatgggaga etgaagatge agtgageeat gaatcageaa etgeacacea gtatgagaga1320
aaaagtggaa ccctatcaca
                                                              1340
```

(2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

gccagattte eggggttttg egggeeeege gatgttttee agaggtttte aagtgggaag 60 aggagagega caaggtgaaa atgeeeegtg eeggggegte eageggagte etgeeagetg120 teeggeggtg gggtggaegt etgatttatg aaggtgeeea teeacetate tgagtaeetg180 aettgtgagg aetgaeaaet aeageateag gtaeaaagtt gttett 226

- (2) INFORMATION ON SEQ ID NO. 53:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 611 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

gcagctgcag cggcagcag ggcagcagag gcagcagcag tagccaccac tccgccgagg 60 ccgcaacccc ggctcgcct ccccaggccc cgccgctgcc gcagtcatgg ctgctgatgg120 ggtggacgaa cgctcgcctc tgctgtcagc atcccactcc ggaaatgtca ctcccaccgc180 cccaccgtac ttgcaagaaa gcagccccag agcggagtcc cacctccata tacagccatt240 gccagtccag acgccagtgg tattccagta ataaactgcc gtgtgtgcca atcactaatc300 aatttggatg gcaagcttca ccagcatgtg gttaagtgca cagtttgcaa tgaagctacg360 ccaatcaaaa acccccaac aggcaagaaa tatgttagat gcccttgtaa ttgtcttctc420 atttgtaagg acacatctcg gcgaatagga tgcccaagac ccaactgtag acggataatt480 aaccttggcc cagtaatgct tattctgaa ggaacaacca gctcagcctg cattgcccaa540 tcccaaccag aagggtacaa gggtcgtgt ttggggcacg gttggggaac acattcctt600 tgggatgga

(2) INFORMATION ON SEQ ID NO. 54:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 689 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```
geogacega egeagggge tggeggaae gtgaagetee geggtgeetg atggeegt 60 tggeggeege gtagetgtt etgttgggg acceecteat teetgeeget geegteeetg120 etgeeteatg geggeeateg gagtteaeet gggetgeaee teageetgtg tggeegteta180 etgttgetae teagaaaatg tggetgeaaa tgatgeeggt gaeegagtta eteetagetgt240 etgttgettae teagaaaatg aagaattgt tggattgea geaaaacaaa gtagaaataag300 ecagtgatee360 aatgatatta aataacateg eggaaagaaa atgtttagte attgaaaaaa atggaaaatt420 accagaagtaa atagataet gagaaagaaa aaaatttgtt ageaaatgaa atggaaaatga aagaaaegga acaattetgta ttgggeteag atggaaage600 ecagtgatee660 eggetagatea atgtttteeg attaattea gaaceggetetg eageteette660 eggetagaaa getggaaaag acteeceta etgetaatgga getggaaaa acteeceta
```

(2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 560 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

agaaaatgga cgctgacatc aatgtcacaa aagcggatgt tgaaaaggcc cgacaacaag 60 ctcaaatacg tcaccaaatg gcagaggaca gcaaagcaga ttactcatcc attctcaga120 aattcaacca tgagcagcat gaatattacc atactcacat ccccaacatc ttccagaaaa180 tacaaagagag cggaggaaag gaggattgtg agaatgggag agtccatgaa gacatatgca240 gaggttgatc ggcaggtgat cccaatcatt gggaagtgcc tggatggaat agtaaaagca300 gccgaatcaa ttgatcagaa aaatgattca cagctggtaa tagaagctta taaatcaggg360 tttgagcctc ctggagacat ttgaatttgag gattacactc agccaatgaa gcgcactgtg420 tcagataaca gcctttcaaa ttccagagga gaaggcaaac cagacctcaa atttggtggc480 aaatccaaag gaaagttatg gccgttcatc aaaaaaaata agcttatgtc ccttttaacg540 gggggcccat tcagcttcag

- (2) INFORMATION ON SEQ ID NO. 56:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 851 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```
gaagaagagt aagaaggaca agaaggccaa agctggtctg gagagcgggg ccgagcctgg 60 agatggggac agtgatacca ccagcaaaag aggtagaatt ggtttctgag tagtgaaggc120 cacttgaagc tggaggagaa actaaagcct tattgagaaa acatgttata gatccttttg180 ttgctgagag agtggaacat aggtcctaga cagggtgaag agttctggca cattttagct240 gctactttga gacctcggtg atgttacctg gtgtggtcat cccatcttgt cctgttttaa300 ggatatgggt ggtgaaagat gaaagaggca gagtttatcc caatgacttc tctgttttgag360 ttgggaagcc tcaccttcag acccagtaac tgtccgcagc tgtctgctag tggttgtctt420 aacatcgtag tcctagtttg catttttaa atcccctctg tttaaaaggt tggtaaaaca480 aggttcactg aattttgtct ctgaattcag tataactgag tttttgtccat gctggtgtct600 gggttatagg cctgatgggc ctggtagttt tccatctgt tctggcctag aggtcagtcc660 tttgcacttc ttgtttaggc ctcgttact tttaaaagat tccacctact tgttttaga accagtaac tgaattctg ctcacctaaa tccacctaga tacttgttcc720, tgtgccctct tgttttag ctcattaaa tcaacttgtt aaggtttaaa aaaaaaaaa840 aaaaaaaaaaa a
```

- (2) INFORMATION ON SEQ ID NO. 57:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1354 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```
cttaccaaca gcctttctgc taagttctgt ttttttggata tttatgactt ggttcatctt 60
attittiteet gattiageag gageeeetti etattieagt tieattitea geatagtage 120
ctttctatac tttttctata agacttgggc aactgatcca ggcttcacta aggcttctga 180
agaagaaaag aaagtgaata tcatcaccct tgcagaaact ggctctctgg acttcagaac 240
attttgtaca tcatgtctta taaggaagcc attaaggtca ctccactgcc atgtatgcaa 300
ctgctgtgtg gctcgatatg atcaacactg cctgtggact ggacggtgca taggttttgg 360
caaccatcac tattacatat tottottgtt tttcctttcc atggtatgtg gctggattat 420
atatqqatct ttcatctatt tqtccaqtca ttqtqccaca acattcaaaq aaqatqqatt 480
atggacttac ctcaatcaga ttgtggcctg ttccccttgg gttttatata tcttgatgct 540
agcaactttc catttctcat ggtcaacatt tttattatta aatcaactct ttcagattgc 600
ctttctgggc ctgacctccc atgagagaat cagcctgcag aagcagagca agcatatgaa 660
acagacgttg teceteagga agacaceata caatettgga tteatgeaga acetggeaga 720
tttctttcag tgtggctgct ttggcttggt gaagccctgt gtggtagatt ggacatcaca 780
gtacaccatg gtctttcacc cagccaggga gaaggttctt cgctcagtat gaagaaaagc 840
aacccaaaac totcaatotg atttgttttt gtttatgtcg atgccotgta gtttgaaagt 900
gaagtaaaga tttagaattc acctaagtcc aaaggaaaac acgtggtttt taaagccatt 960
aggtaaaaaa agttctcaat aaaggcatta caatttttta ggtttagaaa gatggacttt1020
totgataaat ottogooagac atotaaaaaa aaaaccatat tittoacaag aaaatgoaag1080
ttactttttt tggaaataat actcactgat tatggataaa atggaatatt ttcagatact1140
atattggctg tttcaaaata gtactattct ttaaacttgt aatttttgct aagttatttg1200
tctttgttgt atctataaat atgtaaaaaa tatttaaata gatgtacctg ttttgctttc1260
acacttaata aaaaattttt ttttgtaaaa ggaaaaaaaa aagaagagga aaaagaagag1320
aaaggagagg ggaagaaaga ggagaaggca agga
```

(2) INFORMATION ON SEQ ID NO. 58:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

cgtgatctct cctcagtaaa accaaggtgc atttttctgg acccacctat cttgggggtg 60 attaggagta gagggttgta aatacttaaa attttttcc tttctgatat aattattgat120 ctccttctag aagtcctgtc gtctttgctg gagaattttt atttaagcat ccttttgtag180 aagaatctct aatgtccttt tttcatccag atctacactt gatgaatcct aaagctattt240

ctacacagtt cctttattca gttttccc

268

(2) INFORMATION ON SEQ ID NO. 59:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 752 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

tgacaaaaga aatggaataa tttcaaaaaa gttaagtcct gagaagacaa ccctgaaatc 60 tattttgaaa agaaaaggca ccagtgatat cagtgatgaa tctgatgaca ttgaaaatttc120 ttccaagtca agagtaagaa agagagctag ttcattgagg tttaagagaa taaaagaaaac180 caaaaaaggaa cttcacaatt ctcccaaaaa aatgaacaaa acaaaccaag tgtatgcagc240 aaatgaggat cataactctc agtttattga tgattattca tcctcagatg agagtttatc300 cgtcagccac ttcagtttct ctaaaacagag ccacagacca agaactataa gagacagaac360 tagtttttct tcaaaattgc ctagccataa taagaaaaat agcactttta ttccaagaaa420 accaatgaaa tgttcaaaatg aggaaagttg ttaatcaaga gcagtcgtat gaatcaatgg480 ataaattttt agatggcgtt caggaagtgg cttatattca ctcaaaaccag aatgtaattg540 gatcgagcaa agctgaaaat cacatgagcc gatgggcagc acatgacgta tttgagttga600 agcagttttc acagctgaca gcaaccacaa agaaaggcca gcaaccgagt gaaggcagca720 tttcacttcc tctttacatt tcaaatcctg ta

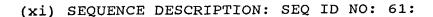
- (2) INFORMATION ON SEQ ID NO. 60:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1389 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

gaactccaag ttagtqgatt gcagaatgga aacttgqctt ttgcggcact gggtgagttt 60 tagtttgtgt gtgtcttgct ggggggtggt gatgattgtc tcagcactca cgcactgcac 120 aaqatqqcaq caqqatacaq cactqcacaa qatqqcaqct cctctqcaqc ttcctcctca 180 geotecotec tigeaccooc acaggitting citiquiquitt tigeaccag taacciacting 240 cctgagatca tgatctctta aaagatgaga ctctcggaag ggttgattgt atgcgtcagt 300 gageetteta teacettetg gaacaaagte acttgaaate tettgatgag attaaggagt 360 ttagtgttac taagaaaatc tgctttgggc cgcagcagtg ctgggtgttc tcagacctga 420 ctgaggaagt tagctgcggg ctgccctgtg ggctggtgct tcaggaggaa tccagagaag 480 tgttcagatg cocccettgg getcetttet satettaate agetetttaa atagetgeee 540 atctcctgtg attgcacaac caagcacttt gacatttgca ccttaggaga ggcagatgtt 600 aaaatggaat ccaaagacca cctagggcgg ggctgggtgg gagatgggag ggccaactgc .660 gagetgetee aetteteage teteccetge cetgeagece tgggceagae aaggeeagaa 720 ggtttcaggg gcatttgaca teccetectg gttctcacca ggaaaacate caaagetttg 780 gaggaaacag gccctgcccc tggctcctta aatgccccgt ctctttgtaa actgatattc 840 agccagcaat gcctaagact tigitaagat cattictact gctitictit cigcticaaa 900 cacacagttc gtctctgagg aaagtaaaat aaatggaata agagtaaatt gggtaaggag 960 atatecaaag etacecagte cettgaceca geacagttgg cegaceegtg teactecetg1020 gctgtcgctg cttctctgtg ctcactgaag ggtgagccag gccagtgctt ccccagcccc1080 tgggcctggt cactacacag tggaaaacag acaagcggcc ccttccccaa atcccaagag1140 tgtcttgctg cttggtgggt gctcatcgca atgttctgaa ggctccaggg ccactttgtt1200 tgtaagtatg atctgggcct caaaatacca tagtagctgc ttgataaaat tctaaaaata1260 tciggttctc tattatgtaa acactattac agtcaccagt gtgtgaagac tcttgagtct1320 ggttctcata tcagagtcat catttttctt cctgtggaat aaaatgcctt gtggacttcc1380 caaaaaaaa

- (2) INFORMATION ON SEQ ID NO. 61:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 726 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

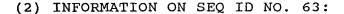


cgtatctgtc cggacggaag caggaagcgg gagcgttagg gccacgcctg cggcgctgct 60 ggttgaggct gtgtgggtgg gggacgggcc gaggcgatgg cggagaagtt tgaccacctal20 qaqqaqcacc tqqaqaaqtt cqtqqaqaac attcqqcaqc tcqqcatcat cqtcaqtqac180 ttccagccca gcagccaggc cgggctcaac caaaagctga attttattgt tactggctta240 caggatattq acaagtgcag acagcagctt catgatatta ctgtaccgtt agaagttttt300 gaatatatag atcaaggteg aaateeceag etetacaeca aagagtgeet ggagaggget360 ctagctaaaa atgagcaagt taaaggcaag atcgacacca tgaagaaatt taaaagcctg420 ttgattcaag aactttctaa agtatttccg gaagacatgg ctaagtatcg aagcatccgg480 ggggaggate accequette ttaaccaqet caecetecet gtgtgaagat cecetgggac540 tgcgatgcgg cgtgaggctg ggactgcgag tgctgacgcc accttcctgc tgaggtggga600 ctgggccctg gacacacccc tcagcccctc tgtcctcatt gttttggcctc atgggaccga660 ggggctggag gagaggcgga gtgtgcccaa gggttcaaga ggttgtttgg ggtgaaatgg720 gtttgt

- (2) INFORMATION ON SEQ ID NO. 62:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - TOPOLOGY: linear (D)
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```
ggctgagaaa aatgggggga gacataacac ccacgaatga aaatacagat ttaagagaag 60
gaaccagtaa agtaggagac agatgtgaag gaaatggaaa tgaggcaaga ggacattggal20
agagagaagt tigotytooa ygagocaggt otggagcato agtytgaggg agttoaggta190
ggctgggcct gtgcctctag gtagggacaa gggaggctgg gtagccaggg ctggtgctta240
aaacccctga ggccatgage teattggetg cetttgtage atcctgtett ettetgtget300
gcctggtttg atctcatctc acctggattc aaagggtaag gtgggcatgg gtcttgggcc360
tgacacccac caaggatgac ctgtggactg ccatcggatg ctgaacaggg agatgaaagg420
aggteetett accataceee tetgecaace ecceagtagg coactgttet gaetttgttt480
ccagaatatc cagaaatcca aaggggctgt tgctgaacag tctgcaggac cagtgacagc540
acctacctgt tgtcccaagg catacaaagg aggcctcaac gctcatgctt ctctaatcaa600
gccctaccaa gacagacaga aaaggaaggg gtagaggaga aggttgaagc tgtggagtta660
gactetgett catteetgaa g
```

681



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1116 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```
gggccacact gagcagattc tttggtagaa ttttcaactt gagactaaca caagtatttc 60
cttttctgtt cagttctcca aatgacaaga agtctttttg ctcaattgaa ggggaatgga 120
atggtgtgat gtatgcaaaa tatgcaacag gggaaaatac agtctttgta gataccaaga 180
agttgcctat aatcaagaag aaagtgagga agttggaaga tcagaacgag tatgaatccc 240
gcagcettig gaaggaigte actiticaact taaaaatcag agacattgai gcagcaactg 300
aagcaaagca caggottgaa gaaagacaaa gagcagaagc cogagaaagg aaggagaagg 360
aaattcagtg ggagacaagg ttatttcatg aagatggaga atgctgggtt tatgatgaac 420
cattactgaa acgtcttggt gctgccaagc attaggttgg aagatgcaaa gtttatacct 480
gatgatcagg gcagtaggca taattcagca acaaacaatc ttcctttggg agaaacctgt 540
tcattccaat cttctaatta cagtggttcc tatctcaggg atactggact ttctgacgca 600
gatgaacaat taaggggaaa agcttccctt ttccctctgt ggcagttacg attttgactt 660
cagteetgag aaaaacttea ggttttgaaa ateagatgat gtetteteet ttteeaaaca 720
ccacacgttg aaagcattta taaatccaag totgaaacto tgogototag tactgotgtt 780
aagatacaca acttgtttct tagttcatat aatctcgggg acacacatac gtatacacac 840
acatacatat atataaatat acctgatgcc agattttttt cataaatatt ctgcctactg 900
taaatatggg ttcctctgag ttgttttaga aaattagcgc aatgtattaa aatcaagtgt 960
taggaaattt catggtctta cctacaataa cttttatttt ggaattgaac tattattaaa1020
ttgtatctaa tcctggaata cagtttaatt aattattctt agtgcttaag gcttcataaa1080
gtaatttttc caaccttttt tttaaaaaaa aaaaaa
                                                                 1116
```

- (2) INFORMATION ON SEQ ID NO. 65:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 806 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

tocaaggget etttagteet teetaageee cacagtaett teeegtagte etgaggettg 60 ggacctcctg gggttcttac cttccctccc cattgctgag acagtctgag aagaggctta120 ggaatttgtc tgtgggagtt tattcatctg tctctcctat ttacctctcc caaaccagga180 tttccacttc tcaaacctgc tgtgatctca caactggagg gaggaagtga gctggggggc240 tcatctccac tggctgcagg aacaggcctc cagggctccc agactgatat tcagactgac300 aatgatttga caaaggaaat gtatgaagga aaagagaatg tatcatttga acttcaaaga360 gacttttccc aggaaacaga cttttcagaa gcctctcttc tagagaaaca acaggaagtc420 cactcagcag gaaatataaa gaaggagaag agcaacacca ttgatggaac agtgaaagat480 gagacaagcc ccgtggagga gtgttttttt agtcaaagtt caaactcata tcagtgtcat540 accatcactg gagagcagcc ctctgggtgt acaggattgg ggaaatccat cagctttgat600 acaaaactcg tgaagcatga aataattaat tctgaggaaa gacctttcaa atgtgaagaa660 ttaqtaqaqc cctttaqqtq tqactctcaa cttattcaac catcaaqaqa acaacactga720 ggaaaagcct tatcagtgtt cggagtgtgg caaagctttc agcattaatg agaaattaat780 ttgqcatcag agacttcaca gtgggg

- (2) INFORMATION ON SEQ ID NO. 67:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 226 base pairs

 - (B) TYPE: Nucleic acid (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

geggateegg egttetgeae tgatettte caagggtgta cagagatgge ggegggtttt 60 eggaaggegg gtaagteeg geagegggaa cacagagage gaageeagtg actacegtaa120 aaaacaaggt aceteaaagg tgtteggaag aagggtgttg aaaaaaaatee agtgagttet180 actacaaaat gactegggtt aaacteeagg gtggggtaca aattat 226

(2) INFORMATION ON SEQ ID NO. 69:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2042 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

gcagccgtcg ccttcggagc gaagggtacc agcccggcag aagctcggag ctctcggggt 60 atcgaggagg caggecegeg ggcgeaeggg egagegggee gggageegga geggeggagg 120 agcoggcage agoggcgogg cgggctccag gcgaggcggt cgacgctcct gaaaacttgc 180 gegegegete gegecactge geceggageg atgaagatgg tegegeeetg gaegeggtte 240 tactecaaca getgetgett gtgetgecat gteegeaceg geaceatect geteggegte 300 tggtatctga tcatcaatgc tgtggtactg ttgattttat tgagtgccct ggctgatccg 360 gatcagtata actiticaag tictgaactg ggaggtgact tigagticat ggatgatgcc 420 aacatgtgca ttgccattgc gatttctctt ctcatgatcc tgatatgtgc tatggctact 480 tacggagcgt acaagcaacg cgcagctgga tcatcccatt cttctgttac cagatctttg 540 actttgccct gaacatgttg gttgcaatca ctgtgcttat ttatccaaac tccattcagg 600 aatacatacg gcaactgcct cctaattttc cctacagaga tgatgtcatg tcagtgaatc 660 ctacctgttt ggtccttatt attcttctgt ttattagcat tatcttgact tttaagggtt 720 acttgattag ctgtgtttgg aactgctacc gatacatcaa tggtaggaac tcctctgatg 780 tectggttta tgttaccage aatgacacta eggtgetget acceeegtat gatgatgeca 840 ctgtgaatgg tgctgccaag gagccaccgc caccttacgt gtctgcctaa gccttcaagt 900 gggcggagtg agggcagcag cttgactttg cagacatctg agcaatagtt ctgttatttc 960 actititgcca tgagcctctc tgagcttgtt tgttgctgaa atgctacttt ttaaaattta1020 gatgttagat tgaaaactgt agttttcaac atatgctttg ctagaacact gtgatagatt1030 aactgtagaa ttetteetgt acgattgggg atataaeggg etteactaae etteectagg1140 cattgaaact teececaaat etgatggace tagaagtetg ettttgtace tgetgggeee1200 caaagttggg cattitictc totgttocot otottttgaa aatgtaaaat aaaaccaaaa1260 atagacaact ttttcttcag ccattccagc atagagaaca aaaccttatg gaaacaggaa1320 tgtcaattgt gtaatcattg ttctaattag gtaaatagaa gtccttatgt atgtgttaca1380 agaatttccc ccacaacatc ctttatgact gaagttcaat gacagtttgt gtttggtggt1440 aaaggatttt ctccatggcc tgaattaaga ccattagaaa gcaccaggcc gtgggagcag1500 tgaccatctg ctgactgttc ttgtggatct tgtgtccagg gacatggggt gacatgcctc1560 gtatgtgtta gagggtggaa tggatgtgtt tggcgctgca tgggatctgg tgcccctctt1620 ctcctggatt cacatececa eccagggeec gettttacta agtgttetge ectagattgg1680 ttcaaggagg tcatccaact gactttatca agtggaattg ggatatattt gatatacttc1740 tgcctaacaa catggaaaag ggttttcttt tccctgcaag ctacatccta ctgctttgaa1800 cttccaagta tgtctagtca ccttttaaaa tgtaaacatt ttcagaaaaa tgaggattgc1860 cttccttgta tgcgcttttt accttgacta cctgaattgc aagggatttt tatatattca1920 tatgttacaa agtcagcaac teteetgttg gtteattatt gaatgtgetg taaattaagt1980 cgtttgcaat taaaacaagg tttgcccaca tccaaaaaaa aaaaaaaaa aaaatggtgg2040

(2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2980 base pairs
 - (B) TYPE: Nucleic acid (C) STRAND: individual (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

agcagagtta gccagaaatg cctcctgctg ccccagcctt agagagctcc catctcaatc attgagectg aaggetteaa geecaagaat geaacaagae eeceageeta eattteteag 120 ctcccctgga gccagctgat cctgtaacgc tgctggaggt cagtctgagc taccaagact 180 gtccctagac aaaggtggag tcccccacac tgcccaagac caaatccctc actcaacctg 240 ctgaggtgtg gatggggaaa cagaggcaaa actgaggcac ctgatgcatt cagcctgctg 300 tgcagcagtg ccattgactg ccctgatgtt cagagagaaa cgcacacaag gtttgcccat 360 gagaattggg gagcagatgg ccaagcagat aggttatgtc tgttttctga gtgatgaagt 420 caggaagccc tgtggctctg gaggccactt gtggttcatt cttttcccat atccttggct 480 tttagaaatg gttaccttca ggacagtgca gctgcattta tcagagcact attgctaagt 540 tttcttttct ggcttgtgtt tttctgggac agtttagaat tgggaggcct attctcatag 600 aacaccaaaa atgatgttca gtgattcatt taacatacac caatgtactc tggctgctgg 660 ggggacaacc ataagcaaga catgcccagg gtttgccgtg gctccagatc tactccctgt 720 aggagttcaa ggatcacaca aacggtagta accagggttg tgaatctgag tacaccctgg 780 caaggettet etteagacty aageageaat tetgecacta ceageageaa eeaggacgte 840 tgttctttgt gggggccaga tcagaagaga gaggcccctg tgacgcccgg gctgcttggt 900 cacaactetg tecaatteaa ggatgtttat eggeetetet tagateetga gtgagacaaa 960 tacagaaatg acccattece tgcccaccag aaactcagag gtgattgggg agactgacacl020 aggaaaatga acttaatcaa gagagactgt gatatgtgct aagaagggtg tgagggaggg1080 agagatgaat titccctgga gggatcctag aaagcattgt catattgcca tctccattag1140 ctcactttta aacaactagg gtgctggaag aacctttgtc tgagggtagt tcatagctgg1200 aaatacttgg aatattttcc agagtctcta aactctcatc ttcccccaca gatacacatc1260 caageteaca aataggagta geaattetag gtggtagggt tgtgtaegga acccetgget1320 gtotgoatat atotoagaat taccocagga coattgtooc aaagtotaga gtotttacag1380 gtaggcaaaa tttgttttca atgcctgtgc ctcagctgct gtcacaaata cccatcttag1440 gatoccatca gottoccato occoaccaga cagocacagt accotoactt totocctatt1500 gttctttcaa atcctgttct caggaaagaa actgccacta attcattcac actaaggtgt1560 aaatgattga taataggaat gagttacctc ttcccacaga catttgtttt taagtatgac1620 agagcagggc cttaatccca agggaaaagg ttatggaact ggagggggtg agctttctgg1680 gtagaaggag actteetgaa ttteettaaa acceagtaag agtaagaeet gttgttttgg1740 aaggtotgot coaccatota agagcactgt tittitittt gttgttgttg ttgttacggt1800 ctctqaqqqa atataqtaaa aatgcatatg cacgtgcaat ttgcacggca gcatttcacc1860 gattgtggac tgtattggct aatgtgtttc ctggtcttta gatgcaaacc attaataaca1920 ctatcttatc tcatagtttt ttcaggggtg cttcttgatt agtagggaat tttgaacacc1980 totttaaata cagotagaaa ataaaaccaa tttgtaaago cacatttgca tatgatgcca2040 gootcacgca tttgtatato tocagaaatt caggtatgco tcaccaattt goocgtottt2100 aataaaatct tgtgttaaaa tttgcatcac gtcgccttcc tatgtatgac gaaacaagaa2160 acagagattt ccaattgctc ttttgtcttc agacatttag taatataaag tacctatttt2220 tatgctgaaa tgtttataca ggtttattaa tagcaagtgc aactaactgg cggcatgcct2280 tgcaacacat titgatatat tagccatgct tccgggtaaa ggcaagcccc aaactcctta2340 tettttgeag tetetetggg atcagtaaaa gaaaaaaaa ataatgtget taagaagtgg2400 gactgtaaat atgtatattt aactttgtat agcccatgta cctaccttgt atagaaaaat2460 aattttaaaa atttgaatgg aagggggtaa aggaggtcat gaagtttttt tgcattttta2520 tttaaatgaa ggaattccaa ataactcacc tacagatttt tagcacaaaa atagccattg2580 taaagtgtta aaatttacga taagtattot attggggagg aaaggtaact ctgatctcag2640 ttacagtttt titttccttt ttaatttcat tattttgggt tttttggtttt tgcagtccta2700 tttatctgca gtcgtattaa gtcctattgc tagaataggt tactacaaaa aaggttatat2760 totgaaagaa aaataactga cattatatat aaccaattaa tttaaagtat tgccatttaa2820 attacacact gagageatgt cetatgeaga catagatttt tetgtteatt tatttttett2880 cattgcagtg gattgatttg ataaatagat gtgttgaatt actacatttg ctgtacatat2940 tatttaataa actttattca gaattgcgtg gcaaaaaaaa

(2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 227 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

cagcattget ccacggcaca gcataaggat agatcccaag tccacagggt ccattttgca 60 ggtcatattc tgatcctagg aaatgtcctt ttcccatagt tgtcctatgc ctttggggtt120 tagtctatcc caggggtaac tgtggagaaa tcattggttt gagagtcaag agagcattgg180 ttttggagct ttaatccctt tctggttgaa ataagggtgt caacttg 227

- (2) INFORMATION ON SEQ ID NO. 75:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 773 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

eggaagtgta aaggtteetg ecteteeteg geeaggegga acetetetge tgggeeeggt 60 ggeegeaaaa gaaetttett teteegeee gaaeggtege egeggeeaae tgeetegeee12% geetegeege etaaecetee ttetetet eteeteteeg gettegegg geeetgeete180 eetetegeee ggeggeatee gettgetget geeaeegeet eeteatette tgeeeggeea240 aceggeetge eeeggtgaag tgatgtgega eaaggagtte atgtgggeee tgaaaaaegg300 agaettggat gaggtgaaag actatgtgge eaaggagaa gatgteaaee ggacaetaga360 aggtggaagg aaaectette attatgeage agattgtggg eagettgaaa teetggaatt420 tetgetgetg aaaggageag atattaatge teeagataaa eateatatta eteetettet480 gtetgetgte tatgaggte atgtteetg tgtgaaattg ettetgteaa agggtgetga540 taagaetgtg aaaggeeag atgteeteg egeetttgaa eeeettetea agggtgetga540 taagaetgtg aaaggeeag atggatgae egeetttgaa geeaetgaea aeeaggeaat600 eaaagetett eteeagtaat ggatggatgg aetgataaet eeggaagaat gaeteteetg660 tggeeteaca etgetgeetg tetgtetgte aeteetetate tgeeagette tteagetaaa720 taetttaaga ggggtgaggg gagagaaaa tteataaeaa ateegaetae eag

(2) INFORMATION ON SEQ ID NO. 77:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 870 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

gacccggcgt ggctactagg agaaggacgt acggtcctgc tagtagagga atatgtcgag 60 tttctctagg gcgccccagc aatgggccac ttttgctaga atatggtatc tcttagatgg120 gaaaatgcag ccacctggca aacttgctgc tatggcatct ataagacttc agggattaca180 taaacctgtg taccatgcac tgagtgactg tggggatcat gttgttataa tgaacacaag240 acacattgca ttttctggaa acaaaatggga acaaaaagta tactcttcgc atactggcta300 cccaggtgga tttagacaag taacagctgc tcagcttcac ctgagggatc cagtggcaat360 tgtaaaacta gctattatg gcatgctgcc aaaaaacctt cacagaagaa caatgatgga420 aaggttgcat cttttccag atgagtatat tccagaagat attcttaaga atttagtaga480 ggagcttcct caaccacgaa aaatacctaa acgtctagat gagtacacac aagaagaaat540 agacgccttc ccaagattgt ggactccacc tgaagattat cggctataag agaataagaa600 ttgcagaaaa taacagtgaa gtgattgaaa ctttcttctg atgagtttct ctaacctaca660 ggatggagta aaacaactgc tacagttcag cacctgtttt atgtgccgaa tcactgtggg720 gaaaggtcag gaaggtgtag tccttcaata ggaaattgta attaaaaatat aacttatatg780 aaccattttt atgtaatctg attagatgt tatagttgat aataataaaa tcacttactt840 ggttgactaa aaaaaaaaa aaaaaaaaa aaagtcgacg

(2) INFORMATION ON SEQ ID NO. 78:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

ttgtgatcgg ctatecttee eggatcaaca gegageecag eeeggteate tacaacegge 60 cogggaacaa cgtgaaactg aactgcatgg ctatggggat ttccaaagct qacatcacqt120

gggagttaac ggataagtcg catctgaagg caggggttca ggctcgtctg tatggaaaca180 qatttotica accccaggga toaatgaccc attcagcatg ccacaaagag gggtggc

- (2) INFORMATION ON SEQ ID NO. 79:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 439 base pairs
 - (B) TYPE: Nucleic acid (C) STRAND: individual

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

gtttgggaag ttgagatttg gagcgaataa gtagggatct ggcaagagga tcatctacct 60 cagtcattag gatttcttaa taaaaaagag attgtatttt tgagttggtt attaagatta120 ttaaaaattag cccttccttt gaaatatgac atcagctttg ctgttctaaa tttaaaaatta180 gttgcttcat cagtagcaca cttccagttt ctataaccaag ccagtcttct cagttttccc240 cttaggatgg gacaagtctg ttcagggggt cattctgtaa ggttcagcag ggggtttggg300 agagggattta aggggaaata cagtggggc agaatgggtt cgggggtaaa ggtaggggac360 aagggagga gggcgaaagg aggggtggaa ggatggggc cttacctaga tcgggggatg420 ccggggggc aaggcaagg

(2) INFORMATION ON SEQ ID NO. 80:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2483 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

gcaaaagtct tcaaactatt gagaaagagc catagactga gtgcaggcac cagtgcgctc ttattactgt gtcaattaaa tgaatgtatt tgaatgtttg gatacttacc tctgaatgta 120 ttttgagtaa taacttcaag tgcaaattat gccatgcata atttctttgg tctcatgttt 180 ttcccccctt ttcttttagg ctttgtcttc tgagtctata gaaaaacttc cagtttttaa 240 caagtcagcc ttcaaacatt atcagatgag ctctgaggct gatgactggt gtatcccaag 300 cagggaacca aagaacctgg caaaagaagt ggccatgtga agagggacac tcaggacact 360 ttacgggatc aaagtgggtc tacaccagtg ctgcttcctg aatgtttgtg tgtgaaccct 420 tgtttcctcc aaaacaaacg acagcaacga aaactcctta atcagaacac tgatecaatg 480 aggaatggag cttgtttctg tgacccagga gaacttagtg caagactaca ggagttaaca 540 gatggccage teettatttt ttaatgtaga ataacteetg agtttatate aaateetgaa 600 qaaataagcc tcagttttcc atctgttttt gataagaata agaaagggag tgagtgtgaa 660 gatggtggtt agcagtttca ctaagactga tattttaggc ctcttgttca catcaaaaga 720 tattggtgtc agaataccag cattttcctg ccatgcaaag gattaaaact tagtttacac 780 tatgtggtta caaatatatg tcaatgtaca ttttgaacat atttatgtgc tatggaagga 840 aatgctggtg actaaaataa ggtttactct gaaagaggag gaattttatt caaagcattc 900 aaacatttta ttcaagtgtt tcaaaattca aagcattgta ttcaaagttg cagtgaaggc 960 atcaacttat gtaaaaactc agaaggaagg ctcctctgat aaaaacacag ctcctttatt1020 atgctgcttt tcttgttcac tttacacact aagtaaacac ttattgtcag gtgcctagtc1080 ttgagtgaat tgttagatgt gcactgaact cgggatgttg gggattggag agagaatt1140 gccaaagtaa cagcaaaaat atctcttact ttgctttgtt tataaataaa ttagtagatt1200 ggaaaaacta gtgttaggga aagaaatcac atgttcagag cctaattcag taggaagggc1260 ttttctctac cctgaaatga aggtaatcca aaggcatcca ttttctaggc ttaaaagata1320 tatttttgat atatttaatg atattctcta cactccagca ttaatatgtc tgtttaaaaa1380 ttactaattc tcaaatggct caagaacatt agaatttaag taccttttag agtaattatt1440ttaagcaaat agcctggacg taagagattc tcatgccagc atgctttcat ttgtcagttg1500 ttgtgactga gagataatga atgacacctg aaatgcatat ggtatttttg ggagagttaa1560 ggtataattt gaaggttggc agaccagttg ggctgattac tcttagagaa gaagaaatgg1620 aaaaatgaaa gaaggcagga aggaaagaaa ggatatagga agagagggaa gcagaaggca1680 tcattggcaa gaggaagaac tggtgttttg aaagcagtat ggattcttta aatgcctctc1800 actottacaa gatagtaggo tttgagataa taaacttaco ogtgtoaatt aacatttaaa1860 ctggcatata gaaaaaaagg aggatttttc tgcattgtaa aataatcagt atggtttata1920 tgttgaattt gacatttgtg tgtaatttca tggtggccta gtgttgtggt gcttctggta1980 atggtaatag aagctcaact attttttgt ggatttcagt ttttatcatc agaagtccta2040 gacagtgaca tttcttaatg gtgggagtcc agctcatgca tttctgatta tacaaaacag2100 tttgcagtag gttatttgtc atttcagttt tttactgaaa tttgagctaa acatttttac2160 atgtaaatac ttgtatttac caaagattta aatcagttga ttaattaatt aactcaaata2220 ctgtgaacta tctttaaaac actagaaaaa agaaatgtta gtatctcaat tacaccaact2280 gtgcaaatga actttgataa aatagaaata atctacattg gcctttgtga aatctgggga2340 agagetttag gattetagta gatggataet gaataeteag geceaettaa tttattaatg2400 tatacattgt gtttttgtct ttatgctatg tacagagaaa tgtgataatt ttttataata2460 aatatttttt atgatgataa aag

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: Nucleic acid (C) STRAND: individual

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ggtggtggg gggggggtgt tgggccaaaa gacttcggta tctgacaaca gcatcatcta 60 cctcagtcat tagggtttct taataaaaaa gaggttgtat ttttgacttg gttattaagg120 ttattaaaat tagcccttcc tttgaaatat gacatcagct ttgctgttct aaatttaaaa180 ttagttgctt catcagtacc acacttccag tttctatacc aagccagtct cctcagtttt240 cccattagaa tygacatyty ctyttcaycy tytcatytct ytaatycttc atycayayay300 tttqqtcata qtattaaaqa gaaaatacaq tqaqqtcaca atqtctccaq aqc

- (2) INFORMATION ON SEQ ID NO. 83:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1039 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

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eggggataac caaacacage tgtttacggt ttctccctta acccatgctt tcataaaccc 60
etteggacag etteccegte caggetttet aaccacacet accecagggg tgeegeatte 120
ctgcactcag aagtctgcag cggtccctca aaaaacttga ttgtgccata aaaatcactg 180
gggatettgt taatacaget tetaaeteaa tagatetggg agateetgea titetaacaa 240
geteccaggt aaggeggagg etgetggtgt gaggaecatg etgtgageag eagggegaga 300
gtgcccaggg ctgatatata ttggaaatat cacccctgaa gccatcgctg gcccccacct 360
cctgtggact gatgccccag ggattcccac cccacttctg caaccccagg tatccttcat 420
tatecacece ateccagaet eccaceceag ggattgeeeg tgaagaettt ggeetageaa 480
attgtgttgg ttatgtgagt gttgttttaa tcagagatgt acatgattgc caatctgcat 540
ttcttaccag tgtgaccaca ctgttacgat gcaattctag ccaaaaaaaa actttttcct 600
agtettatgg aaagcaaata tacaatgatt tteagtagge ttetggaata gaaacagtgg 660
tttgaagacc ccactgccac ctttatggac tggccccttt gagtctgaat ccccggcctc 720
tgtcacctga gacccaaccc ctagctgggc caactccagt gaattcaccc atttttcttc 780
ttcaqaaggc ctttcctgtg tgaqacccac atattttaac cttttgctcc tatcccattt 840
ttaaagaatt agagaataaa ccaggcctgt ttcttttccc ctgaaatccc tgcctctggc 900
ttcctaaacc catcatctaa ggtgacagag cagtgctggg aataggcatc ttcctttcaa 960
ctttcccaaa actggccaca gataggctgg ccatgggaag ggtctttgga tttcggggga1020
ggcaaacgtg ggggattgt
```

(2) INFORMATION ON SEQ ID NO. 85:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

agtgtattca gcaaatgagg gtcagaactt tcagtttatt gatggttatt cagccgcaga 60 tgagagttta tgcgtcagcc acttcaattt ctgtaaacag aggcacaggc caaggactgt120 aaggggcaga actagttttt cttcaaaatt gcctaggcat aataaggaaa atagcacttt180 tatttcaagg aaaccgatgg aatgttcaaa tgaggaagtt gttaatcaag ggcagtcgga240 tggatcaatg ggtaaatttt aggtggcgtc aaggagggc ttatattcac tcaaacccgg300 atgttatttg gtcggccaa ggttggaagg

- (2) INFORMATION ON SEQ ID NO. 86:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 235 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

atttaagtat tttttagttt ttaaaatgtc tttccggtga gggaaggagc cccagccaga 60 aagcaattca atcatggtca agtttccaac tgagtcatct tgtgagtggg taatcaggaa120 aaatgaggat ccaaaagaca aaaatcaaag acagatgggg tctgtgactg gatctttatc180 atccattcta aatccgattg aatattgcgg gcttacaaaa tgccaagggg gtgac 235

- (2) INFORMATION ON SEQ ID NO. 88:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 866 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

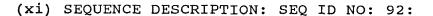
caggaccage ctggccaaca tggcaaaace ctgtctctac taaaaagtaa aaaaaattag 60 ccgggcatgg tggcttgtge ttgtagtece acttcagtet aagtagctgg gactacaggc120 acgtgccaca agcccagcta atgtgggtgt tttgttagag atgaggtagg gccatattgc180 ccaggctcgt cttgaacace ggggctcaag gaatctgccc atcttcgcct cccaaagttc240 tgagatagca agagaagtga caattccact cagtctatta gaggtctgga tataaggga360 ccacacaata actctaactt gacttctaac cattctatct tattgatttg gaggctgtct420 tctgccagat tttttgtggc ttgagatgat attttcgaac ccttctttca ctacctttct480 tacccttaat gtgccaagct tgaaacagga tttgatttc taggctactt ggtcccttc540 tgtgcgtcac caagtaatct ggttcatctt tcgtctcatt cattgtattt tcaagtgaaa600 ttttgtgttc cctttccatg taggtaccaa cttatatga aactcacaat tagggggfcaa gtctctttgg gtgtttttgt tttatgtata taaaaaatgga660 ttttgtgttc cctttccatg taggtaccaa cttatatgga aactcacaat cataatgtaa720 agaagaaatg aaagcctggt gtattgtact tcaagatgcc tccctgatgt ttataaata840 ttttagaatt tttaaatacc aactat

- (2) INFORMATION ON SEQ ID NO. 90:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 846 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

ctecttgtec aaeggaaaaa acatggaagg gttaagecta aaeaaeeete aaaeggaact 60 ttatgecaga aaacaactac ggaataaaaa cecacaaaaaa tacaggaagg aaegttttta120 aeetttaggg cetgegteet etgeetttgg eeeateaggg teaaagagta ggagtgagga180 aggaeggat gggacagea eeeettggae gtteaagtae eteeteagge eteeteagaee tgetgeetttg300 tetetaceaa eettggeagg gatetaggat eeatttagtg ggateaggte eeagteaata360 eeattgggge teaaataagt tettagaace acagagteta gggecagggt eeeaaaeta360 aggtgaeega gtteeettte aagetegtge egaattegge aegageggge aegagettga480 agggaactee gteagetatg agttgggae etggeeetag aetetgtggt tetaagaact540 tatttgagee eeaatggtat tgaetgggae etgateeea eagaegggt eteagateet600 geeaaggttg gtagagacaa ageageaggt etgagagtee taaatggate etaggeegge teeaeteete aagetegga aagggagtee aggaeggtg etetgge660 teeaeteee teetteete aeteeteete tttgaeeetg attgaeege780 aggeeetaaa ggtaaaaaeg teetetetgt attetetgge ttttaeteee tagtgtetet840 geataa

- (2) INFORMATION ON SEQ ID NO. 92:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1374 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library



egaaagegte ggaetacegt tggttteege aactteetgg attateeteg ecaaggaett 60 tgcaatatat ttttccgcct tttctggaag gatttcgctg cttcccgaag gtcttggacg 120 agegetetag etetgtggga aggttttggg etetetgget eggattttge aattteteee 180 tggggactgc cgtggagccg catccactgt ggattataat tgcaacatga cgctggaaga 240 gctcgtggcg tgcgacaacg cggcgcagaa gatgcagacg gtgaccgccg cggtggagga 300 gettttggtg geegeteage geeaggateg ceteacagtg ggggtgtacg agteggeeaa 360 gttgatgaat gtggacccag acagcgtggt cctctgcctc ttggccattg acgaggagga 420 ggaggatgae ategecetge aaateeactt caegeteate cagteettet getgtgacaa 480 egacateaac ategtgeggg tgtegggeat geagegeetg gegeagetee tgggagagee 540 ggccgagacc cagggcacca ccgaggcccg agacctgcat tgtctcctgg tcacgaaccc 600 tcacacggac gcctggaaga gccacggctt ggtggaggtg gccagctact gcgaagaaag 660 ccggggcaac aaccagtggg tcccctacat ctctcttcag gaacgctgag gcccttccca 720 gcagcagaat ctgttgagtt gctgccacaa acaaaaaata caataaatat ttgaaccccc 780 tecceccag cacaaceee ccaaacaac ccaaceeacg aggaccateg ggggcagagt 840 cqttqqaqac tqaaqaqqaa gaqqaqqaqq aqaaqqqqaq tqaqcqqccq cacccaqqqc 900 agagatecag gagetggegg cegeegatea gatggagaag gggggaeeca ggeeageagg 960 agacaggacc cccgaagctg aggccttggg atggagcaga agccggagtg gcggggcacg1020 ctgccgcctt ccccatcacg gagggtccag actgtccact cgggggtgga gtgagactga1080 ctgcaagccc caccetectt gagactggag ctggcgtctg catacgagag acttggttga1140 acttggttgg tccttgtctg caccetcgae aagaccaeae tttgggaett gggagetggg1200 gotgaagttg ctotgtacco atgaactcoo agtttgogaa ttatagagac aatctatttt1260 gttacttgca cttgttattc gaaccactga gagcgagatg ggaagcatag atatctatat1320 ttttatttct actatgaggg ccttgtaata aatttctaaa gcctctgaaa aaaa

(2) INFORMATION ON SEQ ID NO. 93:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 761 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

(2) INFORMATION ON SEQ ID NO. 94:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1825 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

agggaagcta gtagoggaco ggaagtgagg caccotoggg otogagacag oggogacgtt 60 taaagctgag cgacccagtg ccactggaga cggtcagctt ctccactcag gctcctccag 120 cccgagccag aagaccccct cccccagaat tetgggggcc gatggaaggg agccgagtca 180 gategegagg tacccagage egacagaceg gagegacagg gagttgecag aageccegee 240 cctaqqaqtq atcggaaaqc ctcacccatc cqqqtqaqqa acccqqaqqa ccqcctccqq 300 geggagegee gaccatgget acgedectgg tggegggtee egeageteta egettegeeg 360 ccgcggctag ctggcaggtt gtgcgcggac gctgcgtgga acattttccg cgagtactgg 420 agtttctgcg atctctgcgc gctgttgccc ctggcttggt tcgctaccgg caccacgaac 480 gcctttgtat gggcctaaag gccaaggtgg tggtggagct gatcctgcag ggccggcctt 540 gggcccaagt cctgaaagcc ctgaatcacc actttccaga atctggacct atagtgcggg 600 atoccaaggo tacaaagcag gatotgagga agattttgga ggcacaggaa actttttaco 660 aqcaqqtqaa qcaqctqtca qaqqctcctq tqqatttqqc ctcqaaqctq caqqaacttq 720 aacaagagta tggggaaccc tttctggctg ccatggaaaa gctgcttttt gagtacttgt 780 gtcagctgga gaaagcactg cctacaccgc aggcacagca gcttcaggat gtgctgagtt 840 ggatgcagcc tggagtctct atcacctctt ctcttgcctg gagacaatat ggtgtggaca 900 tggggtggct gcttccagag tgctctgtta ctgactcagt gaacctggct gagcccatgg 960 aacagaatcc tcctcagcaa caaagactag cactccacaa tcccctgcca aaagccaagc1020 ctggcacaca tetteeteag ggaccatett caaggacgca eccagaacet etagetggee1080 gacacttcaa tetggeecet etaggeegae gaagagttea gteecaatgg geetecaeta1140 ggggaggcca taaggagcgc cccacagtca tgctgtttcc ctttaggaat ctcggctcac1200 caacccaggt catatctaag cctgagagca aggaagaaca tgcgatatac acagcagacc1260 tagccatggg cacaagagca gcctccactg ggaagtctaa gagtccatgc cagaccctgg1320 ggggaagggc tetgaaggag aacceagttg acttgcetge cacagagcaa aaggagaatt1380 gcttggattg ctacatggac cccctgagac tatcattatt acctcctagg gccaggaagc1440 cagtgtgtcc tecgtetetg tgcagetecg teattaceat aggggaettg gttttagaet1500 ctgatgagga agaaaatggc cagggggaag gaaaggaatc tctggaaaac tatcagaaga1560 caaagtttga caccttgata cccactctct gtgaatacct acccccttct ggccacggtg1620 ccatacctgt ttcttcctgt gactgtagag acagttctag acctttgtga tagaactaaa1680 atgctctctg tactctagtc tcctgcctcc tcagctctgc aagtagttta gtaggaatga1740 agtggaagtc caggettgga ttgcctaact acactgetaa aaatatttgt aatcettaat1800 aattaaactt tggatttgtt aaaaa



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1374 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

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ccgggattcg ccctccgggg agcgattggt cctcgggagg ggcggggagg tggacgcggg 60
taccggcggt cgtcgggtcg gcagcctttg gtcagttggc agcggcaagc gcgctgcggt 120
teeggtggeg ceatgtegtt etgeagette ttegggggeg aggtttteea gaateaettt 180
gaacctggcg tttacgtgtg tgccaagtgt ggctatgagc tgttctccag ccgctcgaag 240
tatgcacact cgtctccatg geoggegtte accgagacea ttcacgccga cagcgtggec 300
aagcgtccgg agcacaatag atctgaagcc ttgaaggtgt cctgtggcaa gtgtggcaat 360
gggttgggcc acgagttcct gaacgacggc cccaagccgg ggcagtcccg attctgaata 420
ttcagcaget egetgaagtt tgteeetaaa ggeaaagaaa ettetgeete eeagggteae 480
taggoggea goocacacc accocagacg gocaccacac tgaggocaca cgttggocat 540
tccaccttgg agttggaacc ctgggcgtcg agacaggaag gcagggcgca gtggttgaaa 600
catcaggaca ctcccaaggc cccggctctg aacaagacct tttcgtttct tggaaaagag 660
actcatttgc tgatggttca tgccttctgc tgggacaggc ctgggctgtg cagccacact 720
gtcggctgac ttagccccct gctcactcta ggtgcctcca ggaggtgagc cctgggtgca 780
getggtetet gaatgaegtt acacceteae ettetttee tggeeetgte tetggaetet 840
cccctgtgag gcccaattcc aagacagact ctcgtcctca ccgaagctta ggcccacatc 900
teccaggetg ettaggagae agaatggaaa eggaggeege eeetgeeage egeeetggee 960
ctggtcactg catgatccgc tctggtcaaa cccttccagg ccagccagag tggggatggt1020
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- (2) INFORMATION ON SEO ID NO. 96:
 - (i) SEQUENCE CHARACTERISTIC:



(A) LENGTH: 2615 base pairs

(B) TYPE: Nucleic acid(C) STRAND: individual(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

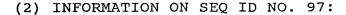
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

cttgggaage teetggatet ttgteaacet gaetgtgega ttetgtatet tgggaaaaga gtccttttat gacacattcc atactgtggc tgacatgatg tatttctgcc agatgctggc 120 agttgtggaa actatcaatg cagcaattgg agtcactacg tcaccggtgc tgccttctct 180 gatocagett ettggaagaa attttatttt gtttateate tttggeacea tggaagaaat 240 gcagaacaaa gctgtggttt tctttgtgtt ttatttgtgg agtgcaattg aaattttcag 300 gtactettte tacatgetga egtgeattga catggattgg aaggtgetea catggetteg 360 ttacactoty tygattocot tatatocact gggatgtttg goggaagoty totcagtgat 420 teagteeatt ceaatattea atgagaeegg acgatteagt tteacattge catateeagt 480 gaaaatcaaa gttagatttt ccttttttct tcagatttat cttataatga tatttttagg 540 tttatacata aattttcgtc acctttataa acagcgcaga cggcgctatg gacaaaaaaa 600 gaaaaagate cactaaaaag aaagatttag atggettett geeagtttga geetaatetg 660 attettacag ttttacette ttgaaceaat gtaaaagttt ttttaatgtt aaatgattaa 720 atticticagtig aggictatictit contitutocco agitaacattic ctigaattitac tigtitatictita 780 ttgtagtact tgcatgacat. ggattcctga tatctgatga gaggttcatt cttgtgtatt 840 cagttaatga caccaaaagg ctcagcccac cccaacccta tctcatgttc agtctgtcta 900 atacatgcca gagatttttt tttcaaaaag tqctttatcc ctacaatgta ctgacagttc 960 ttacagttga gatttgttct tttcagctat tgcttgtgaa aaaaagcaag actatgtcac1020 tctatagaag gctgttaaag tgactcaggc aggaattaat tattctgtac ctaaggggtt1080 acttgtttaa tgggatggca ttgacttttt gaaaatcaag tggactgagt cattgataaa1140 acatttctaa gagtggggct agagaacata ctttacatct gacatccttt ggcctaacaa1200 catctattat tatagtgctc agcagtgtgg gcattgaaga ggcgcagaat gctttgaaag1260 aaactaatca gaatcttgga acatcatgat catgccattc ttaagtaaat caactatttt1320 caacactgaa gaaaaatgaa acattattta gaaaacaatg agattacaag ttccaaactc1380 agccaggaat gtggctcaca cctgtaatcc cagcactttg ggacacctag gtgggagcat1440 cgcttgaagc caggagttca agaccagctt gggcaacgta gtggagaccc ctatctctac1500 aaaaaataaa aaaattagct gggtgtgatg gcacacacct gtttgtccca gctactcaag1560 aagetgagat gggaggatee tgageteagg aggteaagge tgeagtgage egagattgtg1620 ccactgcact gcagcctggg gtgacagtgc aagaccctgt ctcaaaccaa accaaaccac1680 acacacacaa acacacatac acacacaca acacgaggtc caaatggtag cagggatcca1740 aaqqqaacac aqtatgtagg tcaaactggc agtaacagtg tacaqccttt gacaaactag1800 aaatattaga gtaggccaaa cacacctcca aactgtaagg ctgtgcacaa acataaaaaaa1860 tggcagcett ceateteetg caetggetga gtccatttae ttgtgtaett gttetagtga1920 gtggtgggac tgtacatttt tgaatagacc tcaaaaatac ttcattctgc tgctgttcag1980 ttggcttttt aaacctgtct gcagtaggac actgaaaaca gcaagaactt cggggtgaac2040 accogotgat cotttaacaa ggatttotgg caggaaacto acaaaaagga gaactgaaaa2100 tttagacata cagttggcca ttgtaaaaaa catcagtttc ctctcataca ttccaagtaa2160 accaagtaaa ataagtgttg gagtaacact tgcataaaag aatttaagga gtgatagctc2220 tttctgttct gccattccca acattcctgg gggaaaggag actcaatgag ttaatactat2280 ttcactgage ecaagatgga aacttggttt gacetaaaae atetgattaa tataggetag2340 ctgatttctt aaaaattcgt tgcattgaag gatattttgc atgtctgtaa cacctgtcaa2400 tacttgtttg tattgatttc tgatattctt gcagctgact acgtgtaatt gggcagatca2460 gctttgcagt agattatgct gcatcctcgt ggcaaaattc tgtattctta gtgattgtta2520 caaacccctt tattgctgtc tgagaaagtg aaagattgtg tatttctatt aaaacattta2580



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

gttggcagaa acceggatte eggtteeggt gggcetecat cagcaagete cagtgetacg 60 tgteectgge attttaggtg teggttgggt aggcagteat ggateaggta atgcagtttgl20 ttgagcaag teggcagttt gtaaaggaet ceattegget ggttaaaaga tgcactaaacl80 ctgatagaaa agaatteeag aagattgeea tggcaacage aataggattt getataatgg240 gatteattgg ettetttgtg aaattgatee atatteetat taataacate attgttggtg300 getgaataca ttttggaaga gagttttea tettagagat tggtgaacaa gtgtgagggt360 gtgagaaact eacagaatae aaattgeet gtatgttttg tggtgaacaa gtgtgagggt360 eagagatgtt tetatteeta aattaaagta atteaaagt aaaaaaaaa aaaaagtega480 egeggeegeg aatttagtag tagtagg

- (2) INFORMATION ON SEQ ID NO. 98:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3588 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

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(A) ORGANISM: HUMAN

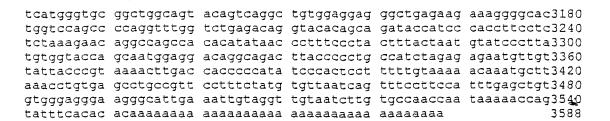
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

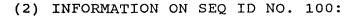
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gagtttgagc tttgagcttg tcttagaaaa taagactgtc cacctgggga ggggagctta 240
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aggaagcaca caaaaaaagc gtcatttaaa accctggata taggctttaa aggatacaaa 480
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tgtgactacc ttgcagagaa catctcaaca gtgcagtaaa atagctctcc tagacttgag 720
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atcagaaagg ttaacatccc tgggaccatt ctacttataa aagagatgaa ctagtgtgct2160
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(2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1218 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

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gtattgtatg agtatttggg tgaagagtac cctgaagtat tgggcagcat tcttggagca 180
ctgaaggcca ttgtaaatgt cataggtatg cataagatga ctccaccaat taaagatctg 240
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tatattggtg aaatgggaaa agactacatt tatgccgtaa caccgttact tgaagatgct 720
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- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1303 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

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gtgctcaaga agtgccttga gttggtgtac agtgccatgg ccagcaagaa tcccagattt 60
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1303
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(2) INFORMATION ON SEQ ID NO. 101:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2333 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

tgaaaaatgc ggacagtata ttcagaaagg ctattccaag ctcaagatat ataattgtga

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attootttoo ogotttgggt occaotgogg cataccagag gagtactgtg tttotggagt 600
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- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1377 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

cattactgtt atatgagaaa cattttagta atttaataaa aggataatgt ttatttaaaa aacctgactt ttccagagta attttgtttt gcacattcat gtttattgaa gtggactaat 120 ttctataatg caaatcagag ttaaatatta aaaattgtgt aaatacaatt gacataggaa 180 ttacattaaa atattaggaa gaaacaagga caaatttaga ccttgaatcc gaagagataa 240 agettaettg aettteaaat ggagagatga tgaaaaccca eteatteagt ettteagaac 300 aaaaagacag tcatctgata agagtatgac atggatgaaa tgccctacag gggccttgga 360 catctttaat ttctgcgatt atgtgaaaga ggtggacttt acagataatg gagcagaagc 420 caacattagt aaaaggaatc ccaacttctt cccatagaat tagaaacatg tgaaagtaca 480 ataaacttct tgttcaaatt accagcatca gagagettee catttgcate tagacettga 540 atttatattt attgatcaag ttctaatttg tatgtatatt ttgtgcatat tcaccaataa 600 cagttaaaat taattatgtg ttatagttaa tatatgcacc taccttcttc cgttagtgca 660 tragtaaatg tgttattttg tratttttcc aaagagagtg ttgtaggttt tccctgtagt 720 totteettta tagettttet tetgataace atgaetteag gagetttaaa actatetate 780 ttgcatttgt gtctggcgga gaactagcca tcagcctcct gaagcctgcc atcattgtta 840 atttgaggac tgggctgtct tggggctcag aaggtaaaga actatttgag cagatgtgtg 900 tgggtggcac tggattccac ccaactgcca agttagtatt gttagagatt tcattttaca 960 acacaaaaat aagcetgtgt caaagatttt aaaatcatgg aaagttaaaa tetagaaaga1020 cottagagaa ccagccaacc aactototoa ttttaaaagt gaaggattoa tagcacagat1080 tacttgccta agatcatcca ggaacgaaga caagaatcca aatgtacttg gggacaagaal140 ttagtcccca aattcagtgt tcttcctagt attaaacatt gcccctttcg acaaattttg1200 gatttcaatc ttggtatatt tcagtaaacc tgctgattta ttaggttact gggtagatgal260 cattagaatg tagatagegt geacgetatg atagaetetg etaagaeatg tteccagtgt1320 ccagcagcaa tgtagatatg tgtgacagtg gtcatgtaga agttataaag cagagta

(2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

ataaggaatg agaagaaagg ctgtgtctta tcagtaggtg agatggaact ggtcctggta 60 gtgttggagc aggacaggca cttagttctg atgctgtggt cctttgtgat agtagagcac120 cggggttaac caccactcct ttaggctact tgtagtgaca acagaagtaa aatatttcaa180 ttatttaatt tagaatgtta tgttttactg gaacctgcaa tatgcatgta cagaattaat240 aatttttact cttttggtca agttatacta aggcaaagcc agtggattca aaagtgagac300 attgacaggc cattt

- (2) INFORMATION ON SEQ ID NO. 104:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2355 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

atgatcatgo cactgoacto catcotgggt gacagoaaga tottgtaaaa aaaaaaaaaa aaaaaaaccag gagtgaaaaa ggaaagtaga aggcagctgc tggcctagat gttggtttgg 120 gaatattagg tgatcctgtt gagattctgg atccagagca atttctttag cttttgactt 180 tgccaaagtg tagatagcct ttatccagca gtattttaag tggggaatgc aacgtgaggc 240 caactgaaca attocccccg tggctgccca gatagtcaca gtcaaggttg gagagtctcc 300 ttccagccag tgacctaccc aaaccttttg ttctgtaaaa ctgctctgga aataccggga 360 agcccagttt tctcacgtgg tttctagctt cttcagactc agcccaaatt aggaagtgca 420 gaagcacatg atggtgaaaa acctaggatt tggcagcctt ccagaatggt atggaatctg 480 agggaagatt tatgtttcgt tttggaggat agctcaagtt gaattttctt tccaqccaqt 540 taccetttea acetacecat actttgtaca actettacae aaataettag atatttatta 600 gatagccctg aattcactct aattataaac agggagtgta aactgccccc agatgttcct 660 gggctgggta aaagcagctg gagtgaagca ctcattttcc ataaaggtaa caaagggcag 720 ctcagtggtt actcaagctc aaaagggttt ttttaagagc aagcattggt taagtctgtg .740 tatactgagt tggaagtgat ttcagcacat tcttttttag tggagtgaaa gttctgaagc 840 coccttttaa cttcctcttg gtttttcatt ataattggta gccatctcat gaactgtctc 900 tgåctgttgt ctctttgtgg tcatgtgatt gtgagcttgc tttctgactt gcatttctga 960 ctttatcctg ttgttaggaa gatagaaact aggttttgaa agattacatg attcaagcga1020 gggattttaa agtaaagatg tatttattct gaagaatcta aaagataaca gattatttgc1080 ttatgaaaga acaatatagt ctgggaatcc cagaatgtca agccaaaggt ctaagaagtc1140 atotoottoa aataotttaa taaagaagta tttogaggag atatotgtoo aaaaaggttt1200 gactggcctc cagattccag ttätttttaa aaagcaactt accactaaat ccttgagtct1260 ccatagagta acagtaaaga aactgatgta acagactctc ctctcaaaagg atctcctctg1320 gaagagacta tcagcggcag cattctccag ggaagaccca tcccctagtg ccagagcttg1380 catcctggag actaaagatt gcactttttt gtagtttttt gtccaaatgc aatcccattt1440 ctgtgcctct tagcatgcag ttagatttgg acaaacaaga ttcctaagga atgactttat1500 taactataat atggttacag ctattatata aatatatat ctggttatag ttctaatatg1560 gagatgttgt gtgcaatgct ggcctgtggt ggtctgtgta atgctttaac ttgtatggag1620 gaggecagge teagagetga gatgtggeet gaacetteee tgtategate etttaattta1680 gaactgtcaa gatgtcactt tctccccctc tgccttttag tggtatctga catatactca1740 aaacagtaat ttcctggtca catcattaac tgctaattct gtatttataa agaattttca1800 gatggacatg tacaaatttg aactcaaacc atccccagtc cagatacagg gcagcgtgta1860 ggtgaccaca ccagagcctc agectcggtc cttctcagcc gtcgggatag gatccaggca1920 tttcttttaa atctcagagg tagcagtaaa cttttcagta ttgctgttag caagtgtgtg1980 tttgccaata gatacccatt atactaatgt gccaagtaaa tgttcattgc acatctgctt2040 ccactgtgtt cccacgggtg ccatgaagtg tgtgaggagc ccctcatctg gagggatgag2100 tgctqcgttg actactgcta tcaggattqt gttgtqtqqa atattcatct acataaattt2160 tatatgcaca gtaatttccc tttttatatg tcaagtaact atttgtaaaa gttatactca2220 caaattatta taatgattac taatatattt tttccatgtt tcattgcctg aataaaaact2280 gtttaccact gttaaaaaaa aaaaagtaaa aaggagggag tgggaaaaaa aagctggggg2340 gggggcccgg tagcc

(2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1339 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

attcggcacg agcatgaaac atgctcattt tacctaacag taaacaagta tgttttgata 60 gatatotgtt aatatgotta tagtggtaag aaatggactt gaggtoccag gagatttoat 120 tttattcacc ctggtcagat acaataaagg ctatgagtat aaatacataa cttcctaacc 180 aggtgtaggg catgttcatg aatatcaaat cttttgatgc tggacccaag agaggaaaag 240 tigtagciaa atgitgatti acttataact agacgictat gigagaaaat ataigtatac 300 atatatatga tatgcagaag tcacttttt tatcaggctt tattctcctt acaaagccac 360 agtttaactg totgcaacag ttggtttatg ttaatgatag acaaataccc agtgtttgtt 420 actttttcca actaccactg taatgataat ctttctcacg tatatacatg caacttcttg 480 getteattte catgaagetg ttteaatata tteagtatae tttgteetta atgetgette 540 tgttaacagt gatctctttc tttttttcat tcttatatct tcattagttc atcataaatc 600 tgtccagttg aggcctcagg accacggcat gatttcatga ctccgaagta ttttacagaa 660 acatttttta aataagggaa atattttata taccagatgg ttcacaagtg atggctcata 720 gctagttttt tttttcttc taaaaaatgt caggttttta aaatcattta ccttattaaa 780 atgaaaagtg ccatacttaa cttttaaagg aaagacctga cttgcttttt ctctatttag 840 actytttttg tactttacta atctttaaac tatcaggaaa aaaaccaaaa ctttatacca 900 atgatttagt aattttgagg catagggtag cttacgtagt ggaggatgtg ccaaatattc 960 tettcaaatg ccacettete aatttataac taaaatagtg ttatetgaet aatteetetg1020 aattttgatg taagatctat ataggccccc aaaatgatcg tagtacatgc cagtcatttc1080 tcagtgaaat aaatacaata ccagagtaca ttatgggttt tattgctttc ttttatggta1140 gacctgttaa tggggaaaaa atacatcaaa tcaaatagaa tcttatatct gtatgttaaa1200 atagageact tacctgaagt cagtggeetg gateatagee etggateatt teccagtetg1260 tectgtgetg ggtggaeett ggaeaaggeg etgeagtagg tgatggetga gageeettee1320 ctgttcccaa gtgccttgt

- (2) INFORMATION ON SEQ ID NO. 106:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3751 base pairs
 - (B) TYPE: Nucleic acid (C) STRAND: individual

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN(C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

gatogogago ggootttgga atotattgog caaaagaagt ttoattttgg ttacttagac ctaaqatcac ttattaaaaa teettatttt eteeaageee ageaaaegtt gaettetggg 120 caaacctgaa aacctgaaaa tgccactttc atgcagtttg tttgaagtta agtggaatcc 180 tttcaaatga cgagctqcag agaactcagc accaagggct gcctatctgt agatagctgt 240 aaaatggaat atttttaaat gaaggcaaat aagtacttaa aagtgagctg agcaataaaa 300 tggtccaata ataggtaaat gcaacagaaa cagaaggaga cctggttgcc ttatgccttt 360 actottacat ggaataaatt cocaatgoat atootatgta aaccataagt gaagggaaat 420 aaacctcgtc atgctccatg ctgtgaggtg tcctttggat attctgtgat gacagagaag 480 cctattttgt tttgttttca gcatctttct ctgatgtacg tttttaagga tttttgtaaga 540 gctgttttca gtgtttaaat tagtgctatt tttccttgtt tttaaaaatg aatctcgtac 600 tgtatcttac tatgtccata cagatgttac aaatcgacag ttttattctt agactcatgt 660 gatecaaget gtatatacea tatataaaea tittaeatga ateatttagt titttaatte 720 atttactaat gctataaaat ttcctatatt accccagtaa tttgcatcag ctggtttata 780 tactaaagca acatgttttg atgagtttct tacatcctta tcgaggaatt gggttaggaa 840 aaaatacata attgtaaaac tgagtttgct gtattatact ttttttcttg agtattagtt 900 gtattactae tcatatgttg attaactgtc tacttaaagt caaggtacct gtatttttaa 960 tocactaatt tittitagt tgggaaatag atticaggic tittattaga ctaacattit1020 ttgagaagta aaattgactt catatacaaa gootgtaatt ttaggogaaa tggaagcaga1080 aatctaggaa gttgtgcttg cttgtatgtt gagtttggtc tcagactaag taatgcatca1140 gaattcatct gtttgaagcc tgaaataatt taggactctg attcactgac caaaagtcag1200 tgttgcagag atttctctac cccgtatggt attttgttag attgttcaac aggaagcaca1260 tgattgagaa catcttggga cagaccaaaa ccactgacag atggcaaggc tcggcgattc1320 tgatttccct tctcaaatct gctcaactcc aagagtcttg agaaactgct aaaattttgc1380 ctctqtcact caagtcttac aaatgttatc ttgtaaacct ttgaggtgaa ctattccact1440 gtottgtaca taggoatott attoactgca coctgtoaca cocagoacco cocgoccogc1500 acattatttg aaagactggg aatttaatgg ttagggacag taaatctact tctttttcca1560 gggacgactg teceetetaa agttaaagte aatacaagaa aactgtetat ttttageeta1620 aagtaaaggc tgtgaagaaa attcatttta cattgggtag acagtaaaaa acaagtaaaa1680 taacttgaca tgagcacctt tagatccctt cccctccatg ggctttgggc cacagaatga1740 acctttgagg cctgtaaagt ggattgtaat ttcctataag ctgtaatagt ggaggtattg1800 tgggttcatt tgagtaagcc ctccaaagat accattcaaa taacctggga gaatgtcata1860 aattattcag ataattaaca ctgcatgaat ctgattcaga ggcatgcatt tacatatgtt1920 geoctaatta ecatttgatg atcataaata caagtgaatg acattggact tttagtaaca1980 aacttaattt ttaaaaaggt gtagacaatg gtggttaaaa aaaaaaaaa aacaggtacc2040 aggttctgtg tgtttgcacc aagtaattga catgtttttt gtttaataca tgtggaccat2100 gaacagtatt cattctactt tttcaaatga tatgctgtag aaaatattcc ttgaagatgt2160 gagatttaaa aatttttccc tttcaatgtt gttttaattg tatttcttac ttggtttttt2220 tgattgatag cacagtgata aatcataata ctagacaaaa ttgtcttctc tttcaaacca2280 gagecatata tatgtetgta tatatgggae etaetgette tetgaggaaa tgeataatet2340 gttaatatca gacaaaatga gcaattggca gtgctcataa tatattccaa tttttattgg2400 aattttcgat ggaatgttat ttcaataaag ccatgtaagg tgaaactttg ataacttttt2460 actottoaag ttagggtaaa ttotgatooa atattoaatt catttgtgta ctoccacatg2520 caaaatgcta aattacaatg cagacattaa gaaaaagtat tgactggagg ggttgaattc2580 cttgagaatt tattttatag tctaaatcac aaatacttta ctcaatttag tttttaaaaat2640 agtaaactga atatttttgt tgtaagccta tcagagtcaa tccttcgttt ggaattgttt2700 tcctgttttt ccttactata aatcatttaa aaactgaatt cattttctta gatggcataa2760 gtctgtctct tgagaaataa gtaaaatact cctattttca gtatctgtag cacctgaaat2820 aggtettigt atagecagaa acaagttatg tigaagttag citticitig icaacagtit2880 tggacaataa aaatctgaaa gtattaacac ttgattttct actggggccc ttcaaacttg2940 gttggaagaa attcaaccag aatatctaca ttagagtata atcatgtgtg gtaggaagat3000 ggactagtta atcaagattt gttgtcactt aaattttttg tgattttttt ccaagccagt3060 ttttttaaat tctaaatgtg ttttgaggta tgggtacatt aattgtaatg taaactatta3120 tacaactgtt tttgcgactt tataggcagg taaattttgc tattactatt gaatacaaat3180 gacaattcat ttatgaccac tcaaacagcg ttagtaacca tttagtgaca aaggattaaa3240 acatccatct ggatgttaat titgaagatg taaattatat gttgtttaaa tttttccagg3300 catctgaaaa ccttatctgc tagacaatgt aagattcaca cagagttatc tgggattctg3360 attititaaa tagtacatat cattaaacca tittictctaa atgtaagaag agcagaaaaa3420 atcttataag attatcagat ttttctaatg acacagaaat gtaagaaaaa aatcccttta3480 tattgaaaaa agatgcagtc aaagtctttt cagacatgcc caaactttga gaatttcttc3540 aaccatctaa tgctataaag atttttgttc ttcctgttca caaccagttg tataacagaa3600

atactageta etgtttteet teetgtgtgt gaagtaatga atcattgatt atgtgaettg3660

ttatgtattc aattaaacac taaagaataa aacattcact cctttaatta ataaaaaaaaa3720

(2) INFORMATION ON SEQ ID NO. 107:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

cgctcggccc ccgcggagag atcgaggtgt acttggccaa gagtctggcg gaaaagctgt 60 atctatgtca gtaccctgtg cgtccagcct cgatgaccta cgatgacatt ccgcacctct120 cagccaagat caagcccaag cagcagaagg tagagcttga gatggccatc gacaccctga180 accccaacta ttgccgcagc aaaggggagc agattgcgct gaacgtggac ggggcctgcg240 ccgacgagac cagcacgtat tcctcgaagc tgatggacaa gcagaccttc tgctcttccc300

- (2) INFORMATION ON SEQ ID NO. 108:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1465 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

gecaacette cetececeaa ecetggggee geoccagggt teetgegeae tgeetgttee teetgggtgt caetggeage cetgteette etagagggae tggaacetaa tteteetgag 120 gctgagggag ggtggagggt ctcaaggcaa cqctgqcccc acqacgqagt qccagqaqca 180 ctaacagtac cottagettg ctttcctcct coctcetttt tattttcaag ttccttttta 240 tttctccttg cgtaacaacc ttcttccctt ctgcaccact gcccgtaccc ttacccqccc 300 egecacetee tigetacece actetigaaa ecacagetgi tigecaggite eccageteat 360 gecageetea teteetttet tgetageece caaagggeet ceaggeaaca tggggggeec 420 agtcagagag ccggcactct cagttgccct ctggttgagt tggggggcag ctctgggggc 480 cgtggcttgt gccatggctc tgctgaccca acaaacagag ctgcagagcc tcaggagaga 540 ggtgagccgg ctgcagggga caggaggccc ctcccagaat ggggaagggt atccctggca 600 gağteteceg gageagagtt cegatgeett ggaageetgg gagagtgggg agagateeeg 660 gaaaaggaga gcagtgctca cccaaaaaca gaagaagcag cactctgtcc tgcacctggt 720 toccattaac gocacotoca aggatgacto egatgtgaca gaggtgatgt ggcaaccago 780 tettaggegt gggagaggee tacaggeeca aggatatggt gteegaatee aggatgetgg 840 agtttatctg ctgtatagcc aggtcctgtt tcaagacgtg actttcacca tgggtcaggt 900 ggtgtctcga gaaggccaag gaaggcagga gactctattc cqatqtataa gaagtatqcc 960 ctcccacccg gaccgggcct acaacagctg ctatagcgca ggtgtcttcc atttacacca1020 aggggatatt ctgagtgtca taattccccg ggcaagggcg aaacttaacc tctctccaca1080 tggaaccttc ctggggtttg tgaaactgtg attgtgttat aaaaagtggc tcccagcttg1140 gaagaccagg gtgggtacat actggagaca gccaagagct gagtatataa aggagaggga1200 atgtgcagga acagaggcgt cttcctgggt ttggctcccc gttcctcact tttccctttt1260 cattcccacc coctagactt tgattttacg gatatcttgc ttctgttccc catggagctc1320 cgaattettg cgtgtgtgta gatgagggge gggggaeggg cgeeaggeat tgttcagace1380 tggtcggggc ccactggaag catccagaac agcaccacca tctaacggcc gctcgaggga1440 agcaccoggo ggtttgggog aagto

- (2) INFORMATION ON SEQ ID NO. 109:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1488 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

cggccggagg agcaggatgg agatecetgt geetgtgeag cegtettgge tgegeegege cteggececg ttgeceggae ttteggegee eggaegeete tttgaecage getteggega 120 ggggctgctg gaggccgagc tggctgcgct ctgccccacc acgctcgccc cctactacct 180 gcgcgcaccc agcgtggcgc tgcccgtggc ccaggtgccg acggaccccg gccacttttc 240 ggtgctgcta gacgtgaagc acttctcgcc ggaggaaatt.gctgtcaagg tggtgggcga 300 acacqtqqaq qtqcacqcqc qccacqaqqa qcqcccqqat qaqcacqqat tcqtcqcqcq 360 egaqttecae egtegetace geetgeegee tggegtggat eeggetgeeg tgaegteege 420 getgtecece gagggegtee tgtecateca ggeegeacea gegteggeee aggeeeeace 480 gecageegea gecaagtagg agggggetgg geegegeeeg caceeeggga geeteeteag 540 gctccctcta ttaaagccga tctgactccg cccagccaga tgtcccgagt gcgccaagga 600 etgteetete acceaeteet ggattetgee etgaceteea teetggacae tgeettgata 660 acatagacce ttecactgae accetegete teagageece tecagettte egaceecaca 720 ccqacaactc cccggcttcc agaccctacc agcactaccc taaccctcag ccgacagtct 780 cagococaco gacocacttt ottggoatat agococactt aagacocoto ototacttoo 840 ttotgagtoc totacaaaga catoogggta ctacatttoc atcoottoco tattttgaca 90% ccaaattatg gtgtagacag ccctggccca accccaggcc agtcaggcac aatcccccca 960 cocccaaac gtcctggact gcacagacct cccactccag accatccagg cctggttccc1020 aagacccgat ccttcccctg caaccagaca gtctacaact gcccctcca gcccattttc1080 tgccgtgaaa ccccagccag ccacaccaga ctctggaacc ctttttcgac tgccccaact1140 cttggacacc aggccaacta gaacacccaa caccaaactg tacagactct cccaccccaa1200 cctccccaga ctctgcacgg atgtcctagg cccctcccc aactctaacc agaccccatc1260 cccctaagtc cctttgtctt gacccccaag tcttcaacca gatatcctcg gcaacccacc1320 teccaecete etectetet cetteaagae ecaactgage accegetetg attecceaca1380 gcctttctcc ctgccaccac tcccttagtc tttcccaggc ttactctccc aataaatgtg1440 ctagagetet gecaaaaaa agaaaaaaa gtegaegegg eeggaatt

- (2) INFORMATION ON SEQ ID NO. 110:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 783 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

(2) INFORMATION ON SEQ ID NO. 111:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1045 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

totgitotgi ggacaactgi tactgitott cogtggccaa coatggeggo caccagecci 60 accoccgote cggccactti coctggacag tgccctcgca ggagtactca caccegotec 120 cgcccacacc ctccgtcccc cagtcccttc ccagcctgc ggtcagagac tggcttgacg 180 cctcccagca gcccggccac caggatttct acagggtgta tgggcagccg tccaccaaac 240

(2) INFORMATION ON SEQ ID NO. 112:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1386 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:

aaaaaa

- (A) ORGANISM: HUMAN
- (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

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cacactcact geocatgaag gaagagggg caagtgtace gaggaagggg atgeeteaca 60
gcaagaggc tgcaccttag gttctgaccc catctgcctc agtgagagcc aggtttctga 120
ggaacaagaa gagatgggag ggcaaagcag cgcggcccag gccacggcca gtgtgaatgc 180
agaggagatc aaggtagccc gtattcatga gtgtcagtgg gtggtggagg atgctccaaa 240
cccggatgtc ctgctgtcac acaaagatga cgtgaaggag ggagaaggtg gtcaggagag 300
tttcccagag ctgccctcag aggagtgaaa gggacaattt ggctgaagtc tttctctgaa 360
aaaagccaaa gggttatagg ggtacactta ggggttgcat gcaagctgtt accaaaaaat 420
ttttaagtat tttcttaatt tgaataataa aaccagagga aatgcataca gggcatgagc 480
aactgaggca aacctttgtg gacatgaatt gttctacgat gaatttttgc tttagtattt 540
taataagaat tacaaagaca atggcatact tggggtgaga gggagctgag gatgtctgag 600
gagggaatag tattgcaggg aagactgaga aaacagtagg atgacagttt tgagtatact 660
ctgcactttt caattgtgca atcttcttgt gcactttaag gctttttaat tttgtttgag 720
aatgcaaatg tatactgtaa gtctaccttt actatctact atgcctactt caccatctct 780
taaggactcg gcatttgtcc acagtcagac tgcaagagag ggtaggtcat gaacagtcac 840
ccgtgctggc tgtagccccc acagaggcaa tcatgcccaa tagattcaag agaagctaag 900
eggaaatgga gggtggaagg tgtgatetgt gggaetgtet gggeetgtta eteateetge 960
tatcaattto ttattaatta atottgatga ttottattaa ttaatcacat ttgcaggaaa1020
ttcagatgag gcaagaaaat tttattggcc tgggtaagac tgaaagcatt ccaaattagg1080
cttagactgt gcaaagggct tagctaagtt atcgagctta aaacccgtca attaaacaaa1140
cattatttga acagttactg catgccacgc actgtgttgg gcttagtaat aaaaaaaaga1200
aaagataagt gcttgttcta gcataaatta aaaggtccaa gggaatttaa tctggaagag1260
aacatatgcc aatttttaaa ctatgacagc tttttttttc tctttccatt caaataggcc1320
```

cgggttcagt cccagaaggg cacaaaatga atgaataaat aaataaatga ataaagacaa1380

(2) INFORMATION ON SEQ ID NO. 113:

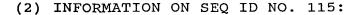
- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1747 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ccagtetgtg agecettgte etgtgggtee ccaeegtetg tegecaatge agtggeaact 60 ggagaggcac acacctatga aagtgaagtg aaactcagat gtctggaagg ttatacgatg 120 gatacagata cagatacatt cacctgtcag aaagatggtc gctggttccc tgagagaatc 180 toctgcagtc ctaaaaaatg toctctcccg gaaaacataa cacatatact tgttcatggg 240 gacgatttca gtgtgaatag gcaagtttct gtgtcatgtg cagaagggta tacctttgag 300 ggagttaaca tatcagtatg tcagcttgat ggaacctggg agccaccatt ctccgatgaa 360 tettgeagte cagtttettg tgggaaacet gaaagteeag aacatggatt tgtggttgge 420 agtaaataca cotttgaaag cacaattatt tatcagtgtg agcotggota tgaactagag 480 gggaacaggg aacgtgtctg ccaggagaac agacagtgga gtggaggggt ggcaatatgc 540 aaagagacca ggtgtgaaac tccacttgaa tttctcaatg ggaaagctga cattgaaaac 600 aggacgactg gacccaacgt ggtatattcc tgcaacagag gctacagtct tgaagggcca 660 tetgaggeae aetgeaeaga aaatggaaee tggageeaee eagteeetet etgeaaaeea 720 aatccatgcc ctgttccttt tgtgattccc gagaatgctc tgctgtctga aaaggagttt 780 tatgttgatc agaatgtgtc catcaaatgt agggaaggtt ttctgctgca gggccacggc 840 atcattacct gcaaccccga cgagacgtgg acacagacaa gcgccaaatg tgaaaaaatc 900 tcatgtggtc caccagetca egtagaaaat geaattgete gaggegtaca ttateaatat 960 ggagacatga tcacctactc atgttacagt ggatacatgt tggagggttt cctgaggagt1020 gtttgtttag aaaatggaac atggacatca cctcctattt gcagagctgt ctgtcgattt1080 ccatgtcaga atgggggcat ctgccaacgc ccaaatgctt gttcctgtcc agagggctgg1140 atggggcgcc tctgtgaaga accaatctgc attcttccct gtctgaacgg aggtcgctgt1200 gtggcccctt accagtgtga ctgcccgcct ggctggacgg ggtctcgctg tcatacagct1260 gtttgccagt ctccctgctt aaatggtgga aaatgtgtaa gaccaaaccg atgtcactgt1320 ctttcttctt ggacgggaca taactgttcc aggaaaagga ggactgggtt ttaaccactg1380 cacgaccate tggetetece aaaageagga teatetetee teggtagtge etgggeatee1440 tggaacttat gcaaagaaag tccaacatgg tgctgggtct tgtttagtaa acttgttact1500 tggggttact ttttttattt tgtgatatat tttgttattc cttgtgacat actttcttac1560 atgtttccat ttttaaatat gcctgtattt tctatataaa aattatata aatagatgct1620 gctctaccct cacaaaatgt acatattctg ctgtctattg ggaaagttcc tggtacacat1680 ttttattcag ttacttaaaa tgatttttcc attaaagtat attttgctac taaataaaaa1740 aaaccgc

(2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1526 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

cgagcccaca ggccccggag tagcagcggg gaggccggga gcccgcggggc cggagccgcc 60 cggccgaggc gtgggggctg cggggccggc ccatccgtgg gggcgacttg agcgttgagg 120 gegegegggg aggegageca ceatgtteag ceageageag cageageage tecageaaca 180 gcagcagcag ctccagcagt tacagcagca gcagctccag cagcagcaat tgcagcagca 240 geagttactg cagetecage agetgeteca geagtececa ceacaggeec gttgecatgg 300 tgtcagcggg ggtcccccgc agcagccaca gcagccgctt ctgaatctcc agggcaccaa 360 ctcaqcctcc ctcctcaacq qctccatqcq qcaqaqaqct ttqcttttac aqcaqttqca 420 aggactggac cagtttgcaa tgccaccage cacgtatgac actgccggtc tcaccatgcc 480 caqueteaca ecoccacaae tggecactee aaatttgcaa cagttettte eccaggecae 600 tegecagtee ttgetgggae etecteetgt tggggteece atgaaccett eccagtteaa 660 cettteagga eggaaceee agaaacagge eeggacetee teetetacca eeeccaateg 720 aaaggattot tottotoaga caatgootgt ggaagacaag toagaccocc cagaggggto 780 tgaggaagcc gcagagcccc ggatggacac accagaagac caagatttac cgccctgccc 840 agaggacate gecaaggaaa aacgeactee ageacetgag cetgageett gtgaggegte 900 cgagetgcca gcaaagagat tgaggagete agaagageee acagagaagg aacetecagg 960 gcagttacag gtgaaggccc agccgcaggc cggatgacag taccgaaaca gacacagaca1020 ccagacctgc tgcctgaggc cctggaagcc caagtgctgc cacgattcca gccacgggtc1080 ctgcaggtcc aggcccaggt gcagtcacag actcagccgc ggataccatc cacagacacc1140 caggtgcagc caaagctgca gaagcaggcg caaacacaga cctctccaga gcacttagtg1200 ctgcaacaga agcaggtgca gccacagctg cagcaggagg cagagccaca gaagcaggtg1260 cagocacagg tacagocaca ggcacattea cagggeecaa ggcaggtgea getgeageag1320 gaggeagage egetgaagea ggtgeageea caggtgeage eccaggeaca tttcacagee1380 cccaqqqcaq qtqcaqctqc aqctqaqqaa qcaqqtccaq acacaqactt ttccacaqqt1440 gcacacacag ggcacagcca agettecagg cacagggage ttettecggg egeggtgtte1500 agtttcaggc caccaggggc agggcc



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1205 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```
cccgagaaaa accaatttaa tgcttctgtt ctcagcattt cacaqcatgc aggactcaaa 60
tggatacaac agaagaaaac aacccacaat ttttggaaaa ccctttgtcc aatgattcat 120
attttgatat ctattgacaa tcccttagaa ctttaaatct caaaaacaaa aaagtactgt 180
ggatctccct cgagccgaat tcggctcgag ggcggtcacc tggagatgag aaaggcccgc 240
ggggggacc atgtgcctgt gtcccacgag cagccgagag gcggggagga cgctgctgcc 300
caggagecca ggeagaggec agagecagag etggggetca aaegagetgt eeegggggge 360
cagaggeegg acaatgeeaa geecaacegg gaeetgaaac tgeaggetgg eteegaeete 420
eggaggegae ggegggaeet tggeeeteat geagagggte agetggeeee gagggatggg 480
gtcatcattg gccttaaccc cctgcctgat gtccaggtga acgacctccg tggcgccctg 540
gatgeccage teegecagge tgegggggga getetgeagg tggtecacag ceggeagett 600
agacaggogo otgggootoo agaggagtoo tagcacctgo tggccatgag ggccacgcca 660
gccactgccc tcctcggcca gcagcaggtc tgtctcagcc gcatcccagc caaactctgg 720
aggicacact cgcctctccc cagggittca tgtctgaggc cctcaccaag tgtgagtgac 780
agtataaaag attcactgtg gcatcgtttc cagaatgttc ttgctgtcgt tctgttgcag 840
ctcttagtct gaggtcctct gacctctaga ctctgagctc actccagcct gtgaggagaa 900
acggcctccg ctgcgagctg gctggtgcac tcccaggctc aggctgggga gctgctgcgt 960
ctgtggtcag gcctcctgct cctgccaggg agcacgcgtg gtcttcgggt tgagctcggc1020
cgtgcgtgga ggtgcgcatg gctgctcatg gtcccaacac aggctactgt gagagccagc1080
atccaacccc acgettgcag tgactcagaa tgataattat tatgactgtt tatcgatgct1140
aaaaa
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(2) INFORMATION ON SEQ ID NO. 116:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3968 base pairs
 - (B) TYPE: Nucleic acid (C) STRAND: individual (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

ggtatttcta aaacataaag aggagaatta agtcagctgc agaacaatgg ggctgattct tctgcttttt ctctggaaaa tctttcattg cttttggtgg aaatttacct agaggttaca 120 accacaggat gtagcttggt ctcttatttg ccttttttggg aaaccaatta ágattaatac 180 aggataaagg aaaaaagcaa totattoatt atataacaca gttgtttgta ttacttgttc 240 cctgcaaagg aaatctgttg aatgcttgca ttttgaattc ttttctaata gaacaaccaa 300 aaaaggcttc ttatggtgca gcaggaaaaa agatcatttt tatagctttg cattcttaac 360 atagcattta aagagcggca tgaattagag gaaagacatg gaacacacag gtagtcggtt 420 tgagatcatc ggcttaaaag tatcctagga tggtaatgac ccagaagtat ttccagttgt 480 ctagtggtgt ggtatgcagg aatgagaagt gttttctttc catttcctgt tggacaggtg 540 gcaatcttag cagagccact atttggagtt gataactaaa gatgcaaata acatgactat 600 gccttctggt catcctagga ctatttggag ttctccaaaa ccttgtaaga ggcatgtcag 660 gcatgcagta aaagcatcta caacttcagc tgggcactgg cagcataggt ctcatcttgg 720 accatacagt cocactttat agaagagggt ggaagttoto caaaacaata tocacaacaa 780 agtotgacot cactotgagg gagatgggaa gtgggaggaa gaaggactaa ccagotocot 870 ggagtaagag gaatttgctt teeetgtetg eecaceaggg getatatgtg eeacetttea 900 ggttggggcc aaggaagtga tgtcagtgtg acagaaggga gagttagacc tccagacgtc 960 agcctccctc ccatggggta cattttcaat ctgagtgttg ttgccttagc tgtgttggta1020 ttagcttgat tggttggtcc gctggttatg aggtgtaggg aggcagtttt tgtttagttt1080 ttaggacttt gcctcttcct ttgtccttag cataatttct aggcagagca tccacgaagt1140 eggtttteat tgecagetea agagegaeaa teatttaega gtteetatgt tatgttaggt1200 gccttatgta tattatccca aatccactgc atggtttaaa tacaggcact ggaatataaa1260 tgaaaaaggt cattacagtc actgactttc tgcaggacct taaacatttc tctttccaca1320 agtttcccct taatcatgtg tcaaacctct cttcctgacg ggaatgttgt gctataatgal380 atctgcataa cgcttgggat tctaggagga aggaaggttc catggacatg taagtacagc1440 atattcccct cagtcttcta ggagggcaga gtgaatccca gaactggtaa gattgggaat1500 ctgagcattg ccactttaat cttagaatat ttatcatttt gacacatcct gttttttaga1560 gaggaaaaca aacacagttt ctgcattggt agtgtaaagc ataccttgtt aggaacgtgt1620 tttgtaagac acatttgggt tgtcattcta gagcatgtca aactttgtac ttcaaaatat1680 atttagtatg attgttagtg gtaacatata tcaaggcttt gaattaactg ttttatttaa1740 ttttcacaag aagcacttat tttagccata ggaaaaccaa tctgagctac aaatagttct1800 ttaaaataaq cccaggttat ttagctattc tagaaaqtqc cqacttcttt caagaagcag1860 gcattgtagg acagctgaga attatcacat agcctaaatt ctagcctggc agcaagagtc1920 acatctgaga tgtccaaaaa aaaaaaaaa aaacacctga tctacattga aagggggtag1980 actaacgtat gtgagaccat tttcctattt gcagttacaa ggttaaaagaa ctttgaaggt2040 catteggety ctaagaggea tytegaacae tetytytyge tettteacay taaaccetec2100 taagagcaga agacacatgg ctgttagtgt ctgcgtttag atttaatttc tcaaataaag2160 geoettgget gegtateatt teatecagtt ataaactagg geteetgeaa geacceceat2220 totaagggtg aattattgaa atcagttgot atttgatgag toacaactgg cocagcaggc2280 agggcatttg aagtcatggt catcaaaaag aaatgattgt tttttgaaaa gctaaatgct2340 taaaatgott otagagggaa gtogtggggo gtgtgotoat tototttaaa atcagggttg2400 ttqaqtttqt ttttaaacat ttttataaqt tcatqaqaaa aaatatataa attctaaqaa2460 ccaacactgt attoccagaa acatgaccct cgctggtctt gggtccacat atcattggac2520 totqqqqqac acaaaqatqc otqtqacact ttqqtqtttqc cqaqttagtc aacaattatt2580

ctgggaaaaa gcagaattga attcttctct agatgtccta ccagggttgg ccaagggcca2640 caaagcaggc taataaattc ccacaggatc cagacaccag gcaaaattgc tctaagaagc2700 cagttactgt catccctcta tggttctaga aaaaatagta caaaaatgac aggtcatcct2760 atgagogtoa tgocaatgaa accocatott otggagaago oottgaatca gaattatott2820 ttttcttgat gtcgtcagat gcagccagtt tcttaatttt tttaaaaaact gtatgtttct2880 gtggtatgta tatttgtaca cctaactacc tggcacttgg aaatcacagc actactcaga2940 ggcaattgaa taaagagaaa tttaatttta aatatcaagt cctgtcaaac atttctcaaa3000 cttctgattt tatcaaaggt ttgccagcca ataaagtgca tcccaagtat acaggggaga3060 aagctagact cctacagggt cctagagttt aagtaatttt tttgttatta atataggtaa3120 taatttttct aattttatt tittggttcc aaatgtaaag ctccttgtgt ttacctctgt3180 ttatgtcatt cttgacatgt ttatctaaat tatgtgtgct ctgtgacagg tgaaatgtaa3240 atotgggato catagtoaag atatoataag gacotactto coagoctaco tttottocto3300 tacctgataa tgataatact caaaataaca acattcaaag gaaacacaaa gaaatcctgc3360 tttcacatct cctatttctt gggctcctta ataactactg atggtttgtt catgaaaaa3420 aatttttaaa tcaaaagatt gtacttggcc ctgagttgaa aaaatttcaa aaatcaaaag3480 tttgtacttg gccctgagtt gaaaaaaaa attcacattc taagaataaa cagaaaaatg3540 ttcttcttgg aagtaaataa caaaagccat agtgttttca tttgtctttt cttcaggata3600 cacggtagaa gtcagagaat ctttgatact tttatttggt gcaataatca aggccatgca3660 acaacccaaa atcaagcatt ttggttcaag tcaggatgac atgagtgggg acagaagctg3720 tggcagtcat tcaaataatc tcatgggtcc tgaggaaaag acaggagtta acgtattaag3780 tttctactat atgcaggaac tgtgttaaat attttacata agttttgata atagctaaca3840 ttagctgagc acaaaatttg ggccctgatt tgtgctgagt atctttcaca gattactgct3900 tttaatcagc agtccttgtg agctaggtat gatcattatc cccatttata gattacggat3960 gagattcg

(2) INFORMATION ON SEQ ID NO. 117:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 798 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

gtaatgggaa atttggtgtg ctgaatctte tteetaggat attgatatat teeaegette 60 tagtgggtat tetgggaatt ttaeeetget cagtatttge cetagggtae tagaaagagg120 agattgteea aacttageag tatggteeat etegtgtaga agtggaaatg teatacagga180 tageaaaaacac tettggttee tttttgeeea ggettgeea gageeggeaa cageaacaaa240 atgtggagga tgeaatgaaa gagatgeaaa ageetetgge eegetatatt gatgaegaag300 atetggatag gatgetaaga gaacaggaaa gagagggga eeetatggee aactteatea360 agaagaataa ggeeaaggag aacaagaata aaaaagtgag acetegetae agtggteeag420 caceteetee eaacagatt aatatetgge etggatateg etggaegga gtggaeagat480 eegettgetae atggaetgtt gaggatatgt aactteetg aggettgegg ggtggetggg600 etgtggtagt gggeatagge ageggatate eeggtgtaa eagttgtetg tgetaataat660 tggageeeae acagaeeag ggtaeetgta ggtaeetgta ggtagettt tgaeeaaga ageggtgttt780 ggtgggtttt eagaggaa 9798

(2) INFORMATION ON SEQ ID NO. 118:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1068 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

eccetetetg tgactcagte tetgagegtt ttaatacgat ggtgteceeg egggatcaaa 60 ettcagegte acagetgagg actggetteg tggteeetga tgggagagea tgaacaggtg 120 gtatgtgaag cccttggaga ccagetette caaagteaaa gecaagacea ttgtgatgat 180 tecegaetee cagaagetee tgegatgtga aettgagtea eteaagagee agttacagge 240 ccagaccaag getttegagt teetgaacca eteagtgace atgttggaga aggagagetg 300 cttgcagcaa atcaagattc agcagcttga agaggtgctg agccccacag gccgccaggg 360 agagaaggag gagcacaagt ggggcatgga gcagggccgg caggagctgt atggggccct 420 gacccaaggc cttcaggggc tggagaagac cctgcgtgac agtgaggaga tgcagcgggc 480 ecgeaceact egetgeetge agetgetgge ecaggagate egggacagea agaagtteet 540 gtgggaggag ctggaactgg tgcgggagga ggtgaccttc atctatcaga agctccaagc 600 gcaggaggat gagateteag agaaettggt gaacatteag aaaatgeaga aaaegeaggt 660 gaaatgccgc aaaatcctga ccaagatgaa gcagcagggt catgagacag ccgcctgtcc 720 ggagactgaa gagataccgc aggagccagt ggctgctgga aggatgacct ccagaaggaa 780 ctgagtgata tatggtctgc tgtgcacgtg ctgcagaact ccatagacag cctcactttg 840 tgctcggggg cctgtcccaa ggcctcgagc ctaagaggcc acaaggggca ccagtgcctg 900 agocctecae teceeteetg ggaetetgae teegaetetg accaggaeet eteecageea 960 cettteagea agagegegee eccetteeca ecegettgag eageegggae tgeteteect1020 gaagacccct ccagagagaa aataaactag cccagaccct cctctaaa 1068

(2) INFORMATION ON SEQ ID NO. 119:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 4584 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ctcgagccgc tcgagccgcg gaagtaattc aagatcaaga gtaattacca acttaatgtt tttgcattgg actttgagtt aagattattt tttaaatcct gaggactagc attaattgac 120 agetgaceca ggtgetacae agaagtggat teagtgaate taggaagaea geageagaea 180 ggattccagg aaccagtgtt tgatgaagct agggcttggg gcaagagggc aagcagcagt 240 tggtggtgaa gataggaaaa gagtccagga gccagtgcga tttggtgaag gaagctagga 300 agaaggaagg agcgctaacg atttggtggt gaaaagagga attgggagtg gtaggatgaa 360 acaatttgga gaagatagaa gtttgaagtg gaaaactgga agacagaagt acgggaaggc 420 gaaqaaaaga atagagaaga tagggaaatt agaagataaa aacatacttt tagaagaaaa 480 aagataaatt taaacctgaa aagtaggaag cagaagaaaa aagacaagct aggaaacaaa 540 aagctaaggg caaaatgtac aaacttagaa gaaaattgga agatagaaac aagatagaaa 6%0 atgaaaatat tgtcaagagt ttcagataga aaatgaaaaa caagctaaga caagtattgg 660 agaagtatag aagatagaaa aatataaagc caaaaattgg ataaaatagc actgaaaaaa 720 tgaggaaatt attggtaacc aatttatttt aaaagcccat caatttaatt tctggtggtg 780 cagaagttag aaggtaaagc ttgagaagat gagggtgttt acgtagacca gaaccaattt 840 agaagaatac ttgaagctag aaggggaagt tggttaaaaa tcacatcaaa aagctactaa 900 aaggactggt gtaatttaaa aaaaactaag gcagaaggct tttggaagag ttagaagaat 960 ttggaaggcc ttaaatatag tagcttagtt tgaaaaatgt gaaggacttt cgtaacggaa1020 gtaattcaag atcaagagta attaccaact taatgttttt gcattggact ttgagttaag1080 attatttttt aaatootgag gactagoatt aattgacago tgacccaggt gctacacaga1140 agtggattca gtgaatctag gaagacagca gcagacagga ttccaggaac cagtgtttga1200 tgaagctagg actgaggagc aagcgagcaa gcagcagttc gtggtgaaga taggaaaaga1260 gtccaggage cagtgcgatt tggtgaagga agctaggaag aaggaaggag cgctaacgat1320 ttggtggtga agctaggaaa aaggattcca ggaaggagcg agtgcaattt ggtgatgaag1380 gtagcaggcg gcttggcttg gcaaccacac ggaggaggcg agcaggcgtt gtgcgtagag1440 gatoctagae cagcatgoca gtgtgccaag gccacaggga aagcgagtgg ttggtaaaaa1500 teegtgaggt eggeaatatg ttgtttttet ggaacttact tatggtaace ttttatttat1560 tttctaatat aatgggggag tttcgtactg aggtgtaaag ggatttatat ggggacgtag1620 geogattice gggtgttgta ggtttetett titeaggett atacteatga atettgtetg1680 aagcttttga gggcagactg ccaagtcctg gagaaatagt agatggcaag tttgtgggtt1740 tttttttttt acacgaattt gaggaaaacc aaatgaattt gatagccaaa ttgagacaat1800 ttcagcaaat ctgtaagcag tttgtatgtt tagttggggt aatgaagtat ttcagttttg1860 tgaatagatg acctgttttt acttcctcac cctgaattcg ttttgtaaat gtagagtttg1920 gatgtgtaac tgaggcgggg gggagttttc agtatttttt tttgtggggg tgggggcaaa1980 atatgttttc agttcttttt cccttaggtc tgtctagaat cctaaaggca aatgactcaa2040 ggtgtaacag aaaacaagaa aatccaatat caggataatc agaccaccac aggtttacag2100 tttatagaaa ctagagcagt tctcacgttg aggtctgtgg aagagatgtc cattggagaa2160 atggctggta gttactcttt tttcccccca cccccttaat cagactttaa aagtgcttaa2220 ccccttaaac ttgttatttt ttacttgaag cattttggga tggtcttaac agggaagaga2280 gagggtgggg gagaaaatg: ttttttctaa gattttccac agatgctata gtactattga2340

caaactgggt tagagaagga gtgtaccgct gtgctgttgg cacgaacacc ttcagggact2400 ggagctgctt ttatccttgg aagagtattc ccagttgaag ctgaaaagta cagcacagtg2460 cagctttggt tcatattcag tcatctcagg agaacttcag aagagcttga gtaggccaaa2520 tqttqaagtt aagttttcca ataatgtqac ttcttaaaag ttttattaaa ggggaggggc2580 aaatattggc aattagttgg cagtggcctg ttacggttgg gattggtggg gtgggtttag2640 gtaattgttt agtttatgat tgcagataaa ctcatgccag agaacttaaa gtcttagaat2700 ggaaaaagta aagaaatatc aacttccaag ttggcaagta actcccaatg atttagtttt2760 tttcccccca gtttgaattg ggaagctggg ggaagttaaa tatgagccac tgggtgtacc2820 agtgcattaa tttgggcaag gaaagtgtca taatttgata ctgtatctgt tttccttcaa2880 agtatagage ttttggggaa ggaaagtatt gaactggggg ttggtctggc ctactgggct2940 gacattaact acaattatgg gaaatgcaaa agttgtttgg atatggtagt gtgtggttct3000 cttttggaat ttttttcagg tgatttaata ataatttaaa actactatag aaactgcaga3060 gcaaaggaag tggcttaatg atcctgaagg gatttcttct gatggtagct tttgtattat3120 caaacttttt toagataaca tottotgagt cataaccago otggoagtat gatggootag3180 atgcagagaa aacagctcct tggtgaattg ataagtaaag gcagaaaaga ttatatgtca3240 tacctccatt ggggaataag cataaccctg agattcttac tactgatgag aacattatct3300 gcatatgcca aaaaatttta agcaaatgaa agctaccaat ttaaagttac ggaatctacc3360 attittaaagt taattgcttg tcaagctata accacaaaaa taatgaattg atgagaaata3420 caatgaagag gcaatgtcca totcaaaata otgottttac aaaagcagaa taaaagcgaa3480 aaqaaatgaa aatgttacac tacattaatc ctggaataaa agaagccgaa ataaatgaga3540 qatqaqttqq gatcaagtqq attgaggagq ctgtgctgtg tgccaatgtt tcgtttgcct3600 cagacaggta totottogtt atcagaagag ttgcttcatt tcatctggga gcagaaaaca3660 gcaggcagct gttaacagat aagtttaact tgcatctgca gtattgcatg ttagggataa3720 gtgcttattt ttaagagctg tggagttctt aaatatcaac catggcactt.tctcctgacc3780 cottocotaq qqqatttoaq gattqaqaaa tttttocato qaqoottttt aaaattqtaq3840 gacttgttcc tgtgggcttc agtgatggga tagtacactt cactcagagg catttgcatc3900 tttaaataat ttcttaaaag cctctaaagt gatcagtgcc ttgatgccaa ctaaggaaat3960 ttgtttagca ttgaatctct gaaggctcta tgaaaggaat agcatgatgt gctgttagaa4020 tcagatgtta ctgctaaaat ttacatgttg tgatgtaaat tgtgtagaaa accattaaat4080 cattcaaaat aataaactat ttttattaga gaatgtatac ttttagaaag ctgtctcctt4140 atttaaataa aatagtgttt gtctgtagtt cagtgttggg gcaatcttgg gggggattct4200 totoctaatot ticagaaact tigtotgoga acactotita aiggaccaga toaggatitig4260 agcggaagaa cgaatgtaac tttaaggcag gaaagacaaa ttttattctt cataaagtga4320 tgagcatata ataattccag gcacatggca atagaggccc tctaaataag gaataaataa4380 cctcttagac aggtgggaga ttatgatcag agtaaaaggt aattacacat tttatttcca4440 gaaagtcagg ggtctataaa ttgacagtga ttagagtaat actttttcac atttccaaaag4500 tttgcatgtt aactttaaat gcttacaatc ttagagtggt aggcaatgtt ttacactatt4560 gaccttatat aggaaaaaga tgag

(2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 982 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

gtggagggga ccctgtggtt agcagcagct atcgcagcgt cggatgttca gagcagcaga 60 agcoggogte gtoggatgtt gtgttgcccg ccaccatgag ctacacaggc tttgtccagg120 gatetgaaac caetttgcag tegacataet eggataecag egeteageee acetgtgatt180 atggatatgg aacttggaac tctgggacaa atagaggcta cgagggctat ggctatggct240 atggctatgg ccaggataac accaccaact atgggtatgg tatggccact tcacactctt300 gggaaatgcc tagctctgac acaaatgcaa acactagtgc ctcgggtagc gccagtgccg360 attecepttit atecagaatt aaccageget tagatatggt geogeattig gagacagaca420 tgatgcaagg aggcgtgtac ggctcaggtg gagaaaggta tgactcttat gagtcctgcg480 actogaggge egteetgagt gagegegaee tgtaceggte aggetatgae tacagegage540 ttgaccetga gatggaaatg geetatgagg geeaataega tgeetaeege gaccagttee600 gcatgcgtgg caacgacacc ttcggtccca gggcacaggg ctgggcccgg gatgcccgga660 gcggccggcc aatggccgca ggctatgggc gcatgtggga agaccccatg ggggcccggg720 gccagtgcat gtctggtgcc tctcggcttg ccctccctct tctcccagaa catcatcccc780 gagtacggca tgttccaggg gcatgcgagg ttggggggcc ttcccgggcg gcttcccgtt840 ttggttttcg ggtttggcaa tggcatgaag cagatgaggg cggactggga agacggggac900 cacagccgat ttgcgaacca agaagaagaa gagaaagcag ggcggcattc tgattgagcc960 982 aqttagcaaa gcagccggaa tt

- (2) INFORMATION ON SEQ ID NO. 121:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 742 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

ctcaacttcg cacqactgcg tgcctcaagc cgacgcagcg gcctactctc gcactgcaga 60 cqqqqaaact gaqqcccqaq gcqqccqqqq tqqqqcaqac ctcccqqcqa gcccqaqccc120 ccqccccqq ctaqccccqc cctqqcccqt aaqaaqcacc cqqqqcqcqa qqcqaaggcq180 cacagegegg ggecaggetg ggtecageag egegatggea geteagegge tgggeaageg240 eqtqctqaqc aaqctqcaqt ctccatcgcq qqcccqcqqq ccaqqqqqca qtcccqqqqq300 gctgcagaag cggcacgcgc gcgtcaccgt caagtatgac cggcgggagc tgcagcggcg360 qctqqacqtq gaqaagtqga tcgacqggcq cctqqagqaq ctqtaccgcq gcatqqagqc420 agacatgccc gatgagatca acattgatga attgttggag ttagagagtg aagaggagag480 aagccggaaa atccagggac tcctgaagtc atgtgggaaa cctgtcgagg acttcatcca540 ggagetgetg geaaagette aaggeeteea eaggeageee ggeeteegee ageeaageee600 ctcccacgac ggcagcctca gccccctcca ggaccgggcc cggactgctc acccctgacc660 ctcttgcact ctccctgccc cccggacgcc gcccagcttg cttgtgtata agttgtattt720 aatggttctg taacaataaa aa

(2) INFORMATION ON SEQ ID NO. 122:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2330 base pairs

 - (B) TYPE: Nucleic acid (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

qtttqqacaa gttqttttaa taggaaatag acctqcqtqc ttcataggtt tcctcaacca 60 cettteetea getttettaa aatgggatet acattggete tteacaceca aatageagae 120 taatcgtttt tetgettage accgtetggt teattgtett gaactetgee ttacageage 180 aagaaaattt tootogacaa gaacotcaat otttagttoo attgagotoo coototggat 240 tttggactta ccagaagtag gaggttctga taccattcaa gatggtcttt ccttcaaagc 300 aggtetgaag aggagactae caaageagtg tttacaaace cagagtecae acaaccatat 360 tgcatagaac agcacttggc tttcacaagc ctcctacagg acctggtgta attggagtga 420 aaqqqcaqaq accetgqaaq tggagqtggc tgtgtgctgc gatgggaaga aggcagaagg 480 cccaggggct ttggacatag agcagggtgg aagctgcaag tactgggaag gaagagagtt 540 tcacagaaac aaagctttgt cacacagaaa tgagttctgt ctcactggtg acttcatccc 600 tcaggctcca gctgagcaga gattttaatc agcttcctta atgggtattg acactgctca 660 ggaagcagta gaccctgtca gggacagcta ttgatctttt gtgttctgat tagattggaa 720 aatagatcaa cttcattgta gtccaggaac tgttggtcac agctactagg aatgaggtga 780 tttctgaggg ctgagaaaaa acacagaatc ttggccagca gccagcagct gcatggtgaa 840 agatgcattc acttctcctt tgagagttgg ggttgagggc aaacatagaa cccaggtttg 900 gettacaace cagtgteecg gaageeetee ttegggagaa etgtaagtaa gaggtgggtg 960 tgtctaaaga caataccatt aatgaatgtt ctggccttac ctaaaaaggt ttagcaattt1020 ggggataact cttggatcta gcttatgtgc gttcacatgc acatttgcta gcccagagct1080 tttaaaatga ggtctggcat atacttgatt acaaatgaaa actcagaaac caattttatt1140 tattaaatca tatettttgt tttteeeeet eeettetaat eeeeeaaagg acetatttga1200 gctgttcccc aattcatctg cttattttgg accatgaatc tgccagagtg atattttctg1260 ttatttctcc tccaaatttt tccctgatgt ttccaataaa gatttacttg ggtggcccct1320 taaggtgaca tcaggatgct cttatgtcct tccagaataa gcatacactt cactcctctc1380 cetticatet cectetgeat tettaattee tigetittet cactiggage egagggtget1440 ttagagaggt ggttttccat gaatcagcca agattcctgt agaagttggg tatacctatt1500 ccagtttcaa ageteetegg etatgetaat gteeceteag agatgaggtt tgaettttag1560 gecegtatga etectecata geetggeeaa ggagaeeatg agtageeatg tetggtttae1620 totttatoot gagactgttt gtttatagot taaaacagaa gtgtgtotto ccagcacaaa1680 cctaatcaat cagtgtatca gtgcatctqq tgqcaacagc tcagcccatt caaagagcaa1740 ggattcagga aaggcacact gatggtgggg agcctcttaa gagcctctaa tgttctccca1800 aaaccagagt tgagagtcgg agtgccagtc gtcggggccc actattcctg aataagggac1860 atgcaagggc cagaagtagc ttgactotog cotaaatato tgtgcctttg cotgtccttt1920 ctcccactct actgaaaccc ggaacagatt cccgcttgcc ttctgatgaa gagaggttag1980 gtaaagagag tttggaggaa aaaagacacc aggaggcagg ctgtggggta ggagagggtt2040 ctgagaggag gcagcaatcc agaatacctc cttttctagc cagcatccct tgaacttttg2100 aaaggttgtg cctaccactg gctggcacac cagggcaatg atttccctgc agaaggaagg2160 aaagaatgtt ttcacccttg catccttctt gggagaagct accagcctgt tgcttcagtt2220 tgagttggtt tcacattcag gattttgggg ttttatgggt tttccttcct ccctgtgttt2280 tgccccqaac gttgatcaac aggggtgaaa aagggccacc tgagggtttc

(2) INFORMATION ON SEQ ID NO. 123:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1860 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

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gaggeagttt gagateacca geattteegt ggatgtetgg cacateetgg aattegaeta 60
tagcaggete eccaaacaaa geategggea gttecatgag ggggatgeet atgtggteaa 120
gtggaagttc atggtgagca cggcagtggg aagtcgccag aagggagagc actcggtgag 180
ggcagccggc aaagagaagt gcgtctactt cttctggcaa ggccggcact ccaccgtgag 240
tgagaagggc acgtcggcgc tgatgacggt ggagctggac gaggaaaggg gggcccaggt 300
ccaggttctc cagggaaagg agccccctg tttcctgcag tgtttccagg gggggatggt 360
ggtgcactcg gggaggcggg aagaggaaga agaaaatgtg caaagtgagt ggcggctgta 420
ctgcgtgcgt ggagaggtgc ccgtggaagg gaatttgctg gaagtggcct gtcactgtag 480
cagectgagg tecagaactt ccatggtggt gettaacgte aacaaggece teatetacet 540
gtggcacgga tgcaaagccc aggcccacac gaaggaggtc ggaaggaccg ctgcgaacaa 600
gatcaaggaa caatgtcccc tggaagcagg actgcatagt agcagcaaag tcacaataca 660
cgagtgtgat gaaggeteeg ageeactegg attetgggat geettaggaa ggagagaeag 720
gaaagectae gattgeatge tteaagatee tggaagtttt aacttegege eeegeetgtt 780
catectcage agetectetg gggattttge agecacagag tttgtgtace etgecegage 840
cocctotgtg gtcagttcca tgcccttcct gcaggaagat ctgtacagcg cgccccagcc 900
agcacttttc cttgttgaca atcaccacga ggtgtacctc tggcaaggct ggtggcccat 960
cgagaacaag atcactggtt ccgcccgcat ccgctgggcc tccgaccgga agagtgcgat1020
ggagactgtg ctccagtact gcaaaggaaa aaatctcaag aaaccagccc ccaagtctta1080.
ccttatccac gctggtctgg agcccctgac attcaccaat atgtttccca gctgggagcal140
cagagaggac atcgctgaga tcacagagat ggacacggaa gtttccaatc agatcaccct1200
cqtqqaaqac qtcttagcca agctctgtaa aaccatttac ccgctggccg acctcctggc1260
caggecacte ceggaggggt egatectetg aagettgaga tetateteac egacgaagae1320
ttcgagtttg cactagacat gacgagggat gaatacaacg ccctgcccgc ctggaagcag1380
qtqaacctga agaaaqcaaa aggcctgttc tgagtgggga gacgccagag gagcctcacg1440
gtcacgtcca acaacaccac tgcaccaggg aaatggatat atatttttgg actggtgttt1500
ttcacaaagt atttttcaat cagagttttc agaacctgac attgttaaag atactgcttg1560
teceggagtt gtgtattttg taaatgttea agggaactgt ttggaaactt ctttecacca1620
ttcaggaggt tatcagaatt aataaaagta tctgttatgt gcacttaagc cgcagctgct1680
atagatagca etgeettett gtteeageta ggeaatgeet ttttttttt tttgaageag1740
ttctctttat aaagtgttat tttgatagtt tgtggattct aaaataccat ataagtcaaa1800
tatggattta acaaagcaat atgtattcat tcactttcga gatttggggg gttgtttttt1860
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(2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 807 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

cotttectea totetattaa attgtaaaca ggactactge atgtactete tttgaggtga 60 atttggaatg gaaggecagg gactatacte tttttaaaat agacatttgt ggggeteaca120 caatatatga aatagtacce tetaaaaaag agaaaaaaa aatcaggegg teaaacttag180 ageaacattg tettattaaa gcatagttta ttteactaga aaaaatttaa tatcaaggac240 tattacatac tecattacta ggaagttett teettaaaaca cacttgatee acateacace etgtttattt teettaaaca teetggaage etaagetett taaaaggetgt ttgcaacttt teettaaaca teetggaage etaagetett taaaaggetgt ttgcacettt aaggacage tgggetgtag tgatteetgg ggccagagtg480 gcattatgtt tttacaaaat aatgacatat gtcacatgtt tgcatgtttg tttgcacetgt gaccaatcat agaaagtatt tgcatgtttg tttgcttgtt540 gatttettga acagecaget tteetgaga tteetgaga tateetggees taacecagttt660 ccatectaat agggaatgga aattaatttt gaaectact gattaacaga teetgagget720 cacattggaa tteeggacag teetgaga

- (2) INFORMATION ON SEQ ID NO. 125:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1932 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 125:

ccqqqqtttt qqqctqqaac tqcaqcqctt aqaqaqctcq qtqqaaqctq ctaaaqqcqq aggegggget etggegagtt eteetteeae etteeeceae eettetetge caacegetgt 120 ttcagcccct agctggattc cagccattgc tgcagctgct ccacagccct tttcaggacc 180 caaacaaccg cagccgctgt tcccaggatg gtgatccgtg tatatattgc atcttcctct 240 ggctctacag cgattaagaa gaaacaacaa gatgtgcttg gtttcctaga agccaacaaa 300 ataggatttg aagaaaaaga tattgcagcc aatgaagaga atcggaagtg gatgagaga 360 aatgtacctg aaaatagtcg accagccaca ggttaccccc tgccacctca gattttcaat 420 gaaagccagt atcgcgggga ctatgatgcc ttctttgaag ccagagaaaa taatgcagtg 480 tatgccttct taggcttgac agccccacct ggttcaaagg aagcagaagt gcaagcaaag 540 caqcaaqcat gaaccttaag cactgtgctt taagcatcct gaaaaatgag tctccattgc 600 ttttataaaa tagcagaatt agctttgctt caaaagaaat aggcttaatg ttgaaataat 660 agattagttg ggttttcaca tgcaaacatt caaaatgaat acaaaattaa aatttgaaca 720 ttatggtgat tatggtgagg agaatgggat attaacataa aattatatta ataagtagat 780 atogtagaaa tagtgttgtt acctgccaag ccatcctgta tacaccaatg attttacaaa 840 gaaaacaccc ttccctcctt ctgccattac tatggcaact taagtgtatc tgcagctcta 900 cattaaaaag gagaaagaga aataacctgt ctctcattcc taagttgcct cattaatttt 960 catqaacaag aatatgtacc tttttgatgc tatattactg cgattaaaaa gttcttgcag1020 gtaatgttta tgatatgtta aacgttgtaa tttcttatcg taattataac attcccattc1080 ttttgtagat gaaacttcta catattgaac cacagatttt ctgagcttct aaatgtagcc1140 tttcattqca catttcaqtq atcaqaataq atatcctttt acacqcacaa aagcaataga1200 ttcattcagt ggacaagttc cttgtttaac tacacagcta tgatggaatg atatatccaa1260 gttccttgcc tcagtgaaat atgcatatgt atatcatgaa agtgggatgc caagtaagct1320 taaaatggca ttctctagca aagagattag acttttaaat aactcttata aaacaggttg1380 gcgatcattt cccaagattg gtttcccttg agtttttgct aaaacaaatc ttagtagttt1440 tgcccgttta aaacaactca caatcgtaaa tgctactatt cctaagatat cttacctttt1500 tatttcagtt tagccatgta ttgtatgagt gtattagtct aagcagtgag aatcttttct1560 atgcctctat tccagcaaaa agtagaagta tcaaataaaa agggcaactt ttaaaatatt1620 aagcetgaag aettetaaaa agacaagaaa catggeetaa ataaccaaca tagatttaca1680 tagtaagttt cacactacet tattaccaaa agcaaacace tettaettta aactacatta1740 tcatgtatat ctattgtatg ctggtcttta ctttttgcca aaatcaacat ataatgaaga1800 ttagaaacat aaaaaaaaa aaaaaaaggo gaccccccga gtagtgggcc cgcgcccggg1920 gatttttccg gg



(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3024 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

atatatgtta agacattccc ttgctaatta ttttcttctc tgttgttcta tttttttggt ccagtttgct gtttttaaag ttttgagtcc cagctggtcc tgtacattta actgaaaaaa 120 aagtaactta aaataatata aaaatagcac tcatgtatgt cctacagtta taggtgaaat 180 ttgatattgt ttgtcttaca tagcatacct atagacagct taagtaaagt gactgttaag 240 agggttatgc ttattgatga actettgtag ttgtttacca getetgttag tatagttaaa 300 ttgatctcag tagcttcaag tatttataaa atggttgaag tccaaataca tgtgataatt 360 acaatacact ttgaattaat ggggggtggg aggctagttg aaatgcattt tatttaccca 420 aggagtatgt taaaatgata gttataaatg ttggaagttt aaagcaagat actcagttta 480 gttctttaca aatcataaga agaacaaaat tagatgttga cattgctatt ttaggctgtg 540 tgttttccat atgcttcttg ctttccctgt cacaggtggt ggcagcaata ttggtgtgat 600 tgaggttatg ctggcaccac tcgcacacag gcgcacaatg gtgttagctg ggcagaaaga 660 gtggcatctc tggctaccgg gctgggggcg acctttacca taggatgaag taaccttgca 720 tteggetgea aggtgtaetg taegtaeaea ggtgetggte gatgteeaet ttetgetttt 780 ctttctttct tttttcttt tttaaagtaa tttcccccac agtaaaatac actgactcct 840 gagtaaattg attttccagt tttatggaat tgggagtctg acaagtgaaa ccaatttaat 900 gtaaagtatt tggctttcaa atggtttctc tgtgctattt tttggaattc tttcagattc 960 cagagatatc ttacgtcttt gattcaattt aaaatttgta cttattttct tttagaaata1020 atgtattgtg tctgtgcaga aaaaaaaaaa ccaaaaagga ttgctttact ccaagaggag1080 agattgtctt aggataaacc tccaagctca catttaatat aacagactga agtaaacatt1140 agaatcctgt ttagagctat tctgcacagt taactactga tctttagaat ctaaaattgt1200 atatgaactt attettaaat aattgaaceg ttttatatte aaatgaetta tgategtggt1260 tagtttggga aaaataagat ggttaaattt tgatttattg aaatgtaatt gtattatttt1320 cataaaatag cattttcatt ttgtaatgtg gtttaacatc cttgttgttt gccaaagaaa1380 tttcatttgg ctgtgaatat tctatttgct tgcagtatct gtttctcttc ctaggctcaa1440 gttggtgacc caagcctatt gtaaacaagt gattatctca aagggagatg ccaatggagt1500 aacaatttgt taaccttacg ttttctgtct gtatattttt ttaaaaatct ggtagtttct1560 ggaaaaaaaa gagaaggggg tttgtagtac ttaaccctat ttatttccgt atattttagt1620 taattagttt ttggaataaa tggatttcag tatagctttg tggttaaatt gcattgcctt1680 tattttatgt ttaggcttat ttttaaatta acatttaaca gaaacatttg aaatagaatt1740 tgcatgtctg ccttaattaa cttaaagact gattttaatc tgactatgac actgagcata1800 ttctttaaat tactcataat ttataatgct taatataatc ttaattaaat ttagcagttt1860 tagtataaga tgtgccattt tgtcctctgt atgtctgaat gaagctataa catttgcctt1920 tttattgcag gttttccttt ggaatatgga taaatacacc atgatacgga aactagaagg1980 acatcaccat gatgtggtag cttgtgactt ttctcctgat ggagcattac tggctactgc2040 atottatgat actogagtat atatotggga tocacataat ggagacatto tgatggaatt2100

tgggcacctg tttcccccac ctactccaat atttgctgga ggagcaaatg accggtgggt2160 acquitctgta tottttagco atgatggact gcatgttgca agcottgctg atgataaaat2220 ggtgaggttc tggagaattg atgaggatta tccagtgcaa gttgcacctt tgagcaatgg2280 tetttgetgt geetteteta etgatggeag tgttttaget getgggaeae atgaeggaag2340 tgtgtatttt tgggccactc cacggcaggt ccctagcctg caacatttat gtcgcatgtc2400 aatccgaaga gtgatgccca cccaagaagt tcaggagctg ccgattcctt ccaagctttt2460 ggagtttctc tcgtatcgta tttagaagat tctgccttcc ctagtagtag ggactgacag2520 aatacactta acacaaacct caagctttac tgacttcaat tatctgtttt taaagacgta2580 gaagatttat ttaatttgat atgttcttgt actgcatttt gatcagttga gcttttaaaaa2640 tattatttat agacaataga agtatttctg aacatatcaa atataaattt ttttaaagat2700 ctaactgtga aaacatacat acctgtacat atttagatat aagctgctat atgttgaatg2760 gaccettttg ettttetgat ttttagttet gacatgtata tattgettea gtagagecae2820 aatatgtatc tttgctgtaa agtgcaagga aattttaaaat tctgggacac tgagttagat2880 ggtaaatact gacttacgaa agttgaattg ggtgaggcgg gcaaatcacc tgaggtcagc2940 agtttgagac tagcctggca aacatgatga aaccctgtct ctactaaaaa tacaaaagaa3000 3024 aaaaaaaaaa aactcgaaac tact

- (2) INFORMATION ON SEQ ID NO. 127:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

ctgcacgggc gcagatgtag gcaccggtcc gagtgcetgc cctctgtccc cgcggctggg 60 tetegtetgc teeggttect gggctcetaa ttettggtcc agettettee aggtetgcg120 gtetgttgtt cccagcgctc tgcgaagetg aaaaggagga gcaacctgtc cagaatcecc180 gcaggacagg aaaaggagg gaaatctcga catggaaaaa ctctacagtg aaaatgaagg240 aatggcttca aaccaaggaa agatggaaaa tgaagaacag ccacaagacg agagaaagcc300 agaaagtaact tgtactetgg aagacaagaa gttagaaaac gagggaaaga cagaaaacaa360 ggcaaaaaca ggaaagtcag ggaaagtcag agagggaggg agagtcagag atggaggagg tcgagagaga480 gggaacccga ggtagggaa gcga

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

PPLLRLFFFY LRKFISTSTA EIRKWYRFGQ IILYEMDPHT TSFLIQARYN IIPGFSKSSQ 60 HGYLCYSVLA FIAASSFRRA FFSKFKLVKV SCLWAAFLPS ITMKMHPTTV RAIIR 115

- (2) INFORMATION ON SEQ ID NO. 129:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

VRDGAPGLSC GFVQNPFILF KSELLVSLRD EETSLSHNLK QLPAARRRPL RLPMATCYSA60 DORRTSPGTV ALVSSMSPSV GV 82

- (2) INFORMATION ON SEQ ID NO. 131:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids

 - (B) TYPE: Protein (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:	
GIITLSLLMI IHPQMEEFIR QPLQFRLKTG AHRTQGTIKE DQEPRFFLSK NWP	53
(2) INFORMATION ON SEQ ID NO. 132:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 52 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:	
LFILRWRSLS VSHFSFVLKQ EPTGPKELLR RTRNLGFFFQ KIGPSPINEG KN	52
(2) INFORMATION ON SEQ ID NO. 133:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 41 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:	

KKKPRFLVLL NSSLGPVGSC FKTKLKWLTD KLLHLRMNNH Q

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 107 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

ADPAFSTDLF QGCTDMAAAF RKAAKSRQRE HRERSSDYRK KQEYLKALRK KALEKNPDEF 60 YYKMTRVKLQ GGVHIIKETK EEVTPEQLKL MRTSGRQIYR KGRGCRS 107

- (2) INFORMATION ON SEQ ID NO. 135:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

RIRRSPLIFS KAVQTWRRLF GRRLSPGSGN TESEAVTTVK NKNTSKLFGR RLLKKIQMNS60 TTK

- (2) INFORMATION ON SEQ ID NO. 136:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

LFWGYFFLSL LNNMYSTLEF NPSHFVVEFI WIFFKSLLPK SFEVFLFFTV VTASLSVFPL60 PGLSRLPKSR RHVCTALEKI SGERRIR 87

- (2) INFORMATION ON SEQ ID NO. 137:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

EANNYMSCQG GSRFHSFSIL PQYPGINAAT GGQSLFVLLP TPSLFCLFNS VKLFCLGPGK60 EPKENLSGQV HFWNAENILK ARFLEYSOLA FFPLI 95

- (2) INFORMATION ON SEQ ID NO. 138:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

DLKQDQGKQK ICIFLKSLGH LLTILLQKTR CSWWSTLSSF ILENIIEIKV SNPTPGYQVK 60 TASLLLGQNC GLLAELFYGL QSKWSYLTHH MTKVLNLVRG KVLNIQFWIQ EIIIVNFPFK120 SMERMLVENI LKI

- (2) INFORMATION ON SEQ ID NO. 143:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 783 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

FLLQPSAFHL YEPPLDYTMT WRMGPRFTML LAMWLVCGSE PHPHATIRGS HGGRKVPLVS 60 PDSSRPARFL RHTGRSRGIE RSTLEEPNLQ PLQRRRSVPV LRLARPTEPP ARSDINGAAV120 RPEQRPAARG SPREMIRDEG SSARSRMLRF PSGSSSPNIL ASFAGKNRVW VISAPHASEG180 YYRLMMSLLK DDVYCELAER HIQQIVLFHQ AGEEGGKVRR ITSEGQILEQ PLDPSLIPKL240 MSFLKLEKGK FGMVLLKKTL QVEERYPYPV RLEAMYEVID QGPIRRIEKI RQKGFVQKCK300 ASGVEGQVVA EGNDGGGGAG RPSLGSEKKK EDPRRAQVPP TRESRVKVLR KLAATAPALP360 QPPSTPRATT LPPAPATTVT RSTSRAVTVA ARPMTTTAFP TTQRPWTPSP SHRPPTTTEV420 ITARRPSVSE NLYPPSRKDQ HRERPQTTRR PSKATSLESF TNAPPTTISE PSTRAAGPGR480 FRDNRMDRRE HGHRDPNVVP GPPKPAKEKP PKKKAQDKIL SNEYEEKYDL SRPTASQLED540 ELQVGNVPLK KAKESKKHEK LEKPEKEKKK KMKNENADKL LKSEKQMKKS EKKSKQEKEK600 SKKKKGGKTE QDGYQKPTNK HFTQSPKKSV ADLLGSFEGK RRLLLITAPK AENNMYVQQR660 DEYLESFCKM ATRKISVITI FGPVNNSTMK IDHFQLDNEK PMRVVDDEDL VDQRLISELR720 KEYGMTYNDF FMVLTDVDLR VKQYYEVPIT MKSVFDLIDT FQSRIKDMEN QKRGVFFEGG780 KTP

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

KMVVGVWVFL RWERMCENLF QGNGFAAEVR MCSCIDLQTP RRWVHTACLG VPRDSRPPTY60 LSEARAAGHG PSAKPVCDAL GALVQEA

- (2) INFORMATION ON SEQ ID NO. 145:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

SFSSLGVRNT LFITFKFALY FFSSMLVLWT FGDVSVRAGE RGVRRPSHRW SWPPPALSSL60 🚤 97 PDHRFPICPS ENLSQGELKF TGQGTSFIYF IMLANRT

- (2) INFORMATION ON SEQ ID NO. 146:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

ASCTKAPRAS HTGLAEGPWP AARASOKYVG GLESLGTPKH AVCTHLLGVC RSIQEHILTS60 AANPEPWKRE SHILSHLKKT HTPTTIE

- (2) INFORMATION ON SEQ ID NO. 147:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

NSKDKCFSLA FITTPETERW RCCASEPRLL ALKHQGHRTQ AWQRGHGQRH ELQTSMLEVS 60 NPLAPPSMQC APTFWVSADR YRNTSLPLQR THFPGKDFHT SSPTSKKPTH PQPFFKAPR 119

- (2) INFORMATION ON SEQ ID NO. 148:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids

 - (B) TYPE: Protein (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

STKGIAHRLG RGAMASGTSF RQVCWRSRIP WHPQACSVHP PSGCLQIDTG THPYLCSEP160 SLEKIFTHPL PPQKNPHTHN HFLKPHG

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

DPPSHSQLGR CCHRMVFESV GARAHFWLSQ QLGWHLLPSA RNSNIMNARD SVLSKVFHPK60 GAGHGCSRL 69

- (2) INFORMATION ON SEQ ID NO. 150:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

SAHLGLPKCW DYRREHPCPA PFGWKTLLST LSLAFIMLLF LALGSKCHPS CCDNQKCALA60 PTLSNTIR 68

- (2) INFORMATION ON SEQ ID NO. 151:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:	
HHTQPIFVFL VATGFHHVGQ AGLEPLTSGD PPTLASQSAG ITGVSTRALP LLDGRLY	57
(2) INFORMATION ON SEQ ID NO. 152:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 57 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:	
SAGIPKLAPK IPLPFSDLLK CYLISGAFPD HTLKTSTPTH GPCPPSRLHF LAYTYQM	57
(2) INFORMATION ON SEQ ID NO. 153:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 32 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:	

(2) INFORMATION ON SEQ ID NO. 154: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 32 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear MOLECULE TYPE: ORF (ii) (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154: TKRAVMKSMH LCAIRAFLVP HSELIDSDYI HF 32 (2) INFORMATION ON SEQ ID NO. 155: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 31 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155: 31 GRVRAVKGRH SDRSHSQQCF QSVNTDEVPT T (2) INFORMATION ON SEQ ID NO. 156: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 52 amino acids (B) TYPE: Protein (C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

VONVMSACNF IFIKAKLIYM EYCSIYYAPI YILSPVVRYF ISLLLNIFYT YL

52

- (2) INFORMATION ON SEQ ID NO. 157:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTFCFFICC IENSHTQFSI LCQCSHHGWT LGRNSPQPFL VSFSQFFSVS RWAPVINLP 59

- (2) INFORMATION ON SEQ ID NO. 158:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

(2) INFORMATION ON SEQ ID NO. 159:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 33 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:	
GSILDMMQEI SSWSQKFPRG AVFLRNGVYL NNS	33
(2) INFORMATION ON SEQ ID NO. 160:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 44 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:	
KKLPGQHGHK LNYYLNKLHF LKIQHLLGTF DSRKRFPASY PKCF	44
(2) INFORMATION ON SEQ ID NO. 161:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 225 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AAGGLGLGVG PRGMWRAGSM SAELGVGCAL RAVNERVQQA VARRPRDLPA IQPRLVAVSK 60 TKPADMVIEA YGHGQRTFGE NYVQELLEKA SNPKILSLCP EIKWHFIGHL QKQNVNKLMA120 VPNLFMLETV DSVKLADKVN SSWQRKGSPE RLKVMVQINT SGEESKHGLP PSETIAIVEH180 INAKCPNLEF VGLMTIGSFG HDLSQGPNPD FQLLLSLPEE TVVKS 225

- (2) INFORMATION ON SEQ ID NO. 162:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CRGPGARRRS PGDVESWQHV GRAGSRVRIA GGERARAAGC GAAAAGSPSH PAPASGGQQN60 QTCRHGDRGL WTWAAHFWRE LRSGTARKSI KSQNSVFVS 99

- (2) INFORMATION ON SEQ ID NO. 163:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

LRSCPKLPMV ISPTNSRLGH LAFMCSTMAM VSEGGRPCLL SSPLVLIWTI TFNLSGEPFL 60 CQELFTLSAN FTESTVSSMK RLGTAINLLT FCFCRWPMKC HLISGHKDRI LGFDAFSSSS120

(2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

TSTGPSSPLV ASAATELAAF AAAFSSACMR PEGSASLFWN RLPLLMFGDL QGCEAREGIA60 MRILQASFSG LSSKG

- (2) INFORMATION ON SEQ ID NO. 165:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

NTHGDALTCL TPLQVPKHEE GKAIPKQRGR TFRAHTCRAK GSGKSCQFSC SRGYQGAGGT60 SAGLALYLHT RTAASRGTSG SPVGSVAPQQ 90

- (2) INFORMATION ON SEQ ID NO. 166:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

SHPFEDSPEK EACKIRMAMP SRASHPCRSP NMRRGRRFQN REAEPSGRIH AELKAAAKAA60 SSVAAEATRG LEGPVLV 77

- (2) INFORMATION ON SEQ ID NO. 167:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 347 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

TAFPLPVVVA AVLWGAAPTR GLIRATSDHN ASMDFADLPA LFGATLSQEG LQGFLVEAHP 60 DNACSPIAPP PPAPVNGSVF IALLRRFDCN FDLKVLNAQK AGYGAAVVHN VNSNELLNMV120

WNSEEIQQQI WIPSVFIGER SSEYLRALFV YEKGARVLLV PDNTFPLGYY LIPFTGIVGL180 LVLAMGAVMI ARCIQHRKRL QRNRLTKEQL KQIPTHDYQK GDQYDVCAIC LDEYEDGDKL240 RVLPCAHAYH SRCVDPWLTQ TRKTCPICKQ PVHRGPGDED QEEETQGQEE GDEGEPRDHP300 ASERTPLLGS SPTLPTSFGS LAPAPLVFPG PSTDPPLSPP SSPVILV 347

- (2) INFORMATION ON SEQ ID NO. 168:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 588 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

QVTNMSDKSE LKAELERKKQ RLAQIREEKK RKEEERKKKE TDQKKEAVAP VQEESDLEKK 60 RREAEALLQS MGLTPESPIV PPPMSPSSKS VSTPSEAGSQ DSGDGAVGSR RGPIKLGMAK120 ITQVDFPPRE IVTYTKETQT PVMAQPKEDE EEDDDVVAPK PPIEPEEKT LKKDEENDSK180 APPHELTEEE KQQILHSEEF LSFFDHSTRI VERALSEQIN IFFDYSGRDL EDKEGEIQAG240 AKLSLNRQFF DERWSKHRVV SCLDWSSQYP ELLVASYNNN EDAPHEPDGV ALVWNMKYKK300 TTPEYVFHCQ SAVMSATFAK FHPNLVVGGT YSGQIVLWDN RSNKRTPVQR TPLSAAAHTH360 PVYCVNVVGT QNAHNLISIS TDGKICSWSL DMLSHPQDSM ELVHKQSKAV AVTSMSFPVG42Q DVNNFVVGSE EGSVYTACRH GSKAGISEMF EGHQGPITGI HCHAAVGAVD FSHLFVTSSF480 DWTVKLWTTK NNKPLYSFED NADYVYDVMW SPTHPALFAC VDGMGRLDLW NLNNDTEVPT540 ASISVEGNPA LNRVRWTHSG RGGGCGGILK DKFCYFAMLG GAVCWSPQ 588

- (2) INFORMATION ON SEQ ID NO. 169:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

FHVEQLSHSF LSWRKDTIQR GSKDFVKRGI HNLLWSKCPH L

41

- (2) INFORMATION ON SEQ ID NO. 170:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

- (2) INFORMATION ON SEQ ID NO. 171:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KAFLVLSFPK WALFLVIHMT LFGCGCLLNF LFWTSFSKPK PARDRKGNGN

50

- (2) INFORMATION ON SEQ ID NO. 172:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CTFNIESFIY LIVYRTFHNY THLLHNILTS IFKFFCTSSF SFNLVKPVIH TNVYCELSEG60

- (2) INFORMATION ON SEQ ID NO. 173:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

EESFVFLIHS FVNRYKGTNV LTYTKKKKIL VYPLMLIHRV LSYNVIQLGS LTFFPKNIFI60 EKGITLS

- (2) INFORMATION ON SEQ ID NO. 174:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

LYHIIRKHSV DOHKWVHKNF FFLGVCKHIC SFISVYKTVN QKDKTFFLVF VIFFLN 56

- (2) INFORMATION ON SEQ ID NO. 181:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 289 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SRRTQGAAST RFPQPDTIGQ DFSASAQRGG LVAHSDLDER AIEALKEFNE DGALAVLQQF 60 KDSDLSHVQN KSAFLCGVMK TYRQREKQGT KVADSSKGPD EAKIKALLER TGYTLDVTTG120 QRKYGGPPPD SVYSGQQPSV GTEIFVGKIP RDLFEDELVP LFEKAGPIWD LRLMMDPLTG180 LNRGYAFVTF CTKEAAQEAV KLYNNHEIRS GKHIGVCISV ANNRLFVGSI PKSKTKEQIL240 EEFSKVTEGL TDVILYHQPD DKKKNRGFCF LEYEDHKTAA QARRRLIEW 289

(2) INFORMATION ON SEQ ID NO. 182:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 39 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:	
KLCTEWLKVG GIWRWMRGSC LGRLCFTWIR VGLREEIGV	39
(2) INFORMATION ON SEQ ID NO. 183:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 42 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:	
EAVMTLILIL HTYFLTQPYS NPSEAKPSQT APSHPSPYPP NL 4	12
(2) INFORMATION ON SEQ ID NO. 184:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 60 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	

(iii) HYPOTHETICAL: yes

(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:	
PSFSFYTPIS SRNPTLIQVK QSLPRQLPLI HLHIPPTFNH SVHNFYSLHT SYLLI	FLTNK6
(2) INFORMATION ON SEQ ID NO. 188:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 46 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:	
RSRFHMMLTL RALQLSLPTK IGGACFRVSR LSPTEKKKKK MSLEEA	46
(2) INFORMATION ON SEQ ID NO. 189:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 65 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	

ITFSHDAHAQ GASIIPPHKD RWRVFQGLSS LSYRKEKEKN VIRRGVTRQS VPRFVFPGVA60 65 ERDQF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

- (2) INFORMATION ON SEQ ID NO. 190:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 66 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ECREAGPLFL QSRLELISFG HSRKHKPGDG LTCYASSNDI FFFFFSVGER RETLKHAPP160 FVGRDN 66

- (2) INFORMATION ON SEQ ID NO. 191:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

RQTEGETEML RKPSYTTLPR NTSLRECKKY YWRWKSRKTA MGRRPRGD

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- (2) INFORMATION ON SEQ ID NO. 192:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

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OR:	IGIN	
(A)	ORGANISM:	HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

RAETRSQGQL NEDKLKGKLR CLESPAIQLY PEILPLGNVK STTGDGRAEK QLWAEGQGVI60

- (2) INFORMATION ON SEQ ID NO. 193:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

SCIAGLSKHL SFPFSLSSLS CPWLRVSALQ LLPLRAFPPA SDLL

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- (2) INFORMATION ON SEQ ID NO. 194:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EIMNGLVLDN IWPHKLLTSV LGESHFVNHT SEIYMMLNGE QRRSCCKRCI KYLCCFCMRL60 RSFSHLSPLF PIRISREAKL FCGFGNGHFP GKCIWIDD 98

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- MOLECULE TYPE: ORF (ii)
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AHSSTKAKSK SEFLPILPLC NTLRSSHNCP TPHLPVSCCT KSPSLSSFRY IVRQGRRALR 60 RRAFEALSTL PASVKMRLHY SPEKRARFSH RSRCIFPGND HSQTHRTVWL LWISL

- (2) INFORMATION ON SEQ ID NO. 196:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

SGVKRISCVL ETKAYCHCFK KSLCEMKKNM TNTGSHTYTY IQRNLHTCTH TGRYRHTVPP 60 KRSPNQSSYR FYHSVILSEV PTTAQHLTYP FPAAQSLLHS HLFDTSSGRA EGHYAAEHSR120 LSAHCQPA

- (2) INFORMATION ON SEQ ID NO. 200:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

RPGVEPPLLR RLPDSETQKR VQGWGEMWSE GRFAFEKGSS RTHWDIVTHL NHLLIERCWP60 PNNGRSGPGP RA

- (2) INFORMATION ON SEQ ID NO. 201:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

GPSPYARGPG PDLPLLGGQH LSIRRWFKCV TMSQCVLELP FSNANLPSLH ISPHPWTRFC60 VSESGNLLKR GGSTPGL

- (2) INFORMATION ON SEQ ID NO. 202:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

EANTFLSEDG SNVLQCPSVF SNFLSQMQTF PHSTSLPIPG PVSVSLSQAT FSKEGVPLPA60

(2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

PTTTLVIPLF FLSSRKRKQK DSFQTALCSL HCSFPKQAAS TGKAHVVTPY FSEVLLFHGV60 TLLSESKFRK QVLPLADKNH TSFL 84

- (2) INFORMATION ON SEQ ID NO. 204:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CDRVPLFLSY WCAVADSWLT ASSVSHVKGI LSPQPTECAP PGPANCFFNF FFFFFFLVET 60 GSPSVAQDGL ELLGSSNPPT LASQSAEITG MSHYAQPEQD DLNLINSTPK QQLSLSQGCQ120 GGLCEGKD

- (2) INFORMATION ON SEQ ID NO. 205:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

WVAGRRHLLS VQTKSLQVLG LDLCVTPESQ CIRYLYKKLV WFLSAKGKTC FLNLLSDNKV60 TPWKRRTSEK YGVTTWAFPV LAACFGKLQC RLQRAV 96

- (2) INFORMATION ON SEQ ID NO. 206:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

PDFRGFAGPA MFSRGFQVGR GERQGENAPC RGVQRSPASC PAVGWTSDL

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- (2) INFORMATION ON SEQ ID NO. 207:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

(2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CCSCQSSQVR YSDRWMGTFI NQTSTPPPDS WQDSAGRPGT GHFHLVALLF PLENLWKTSR60 GPQNPGNL 68

- (2) INFORMATION ON SEQ ID NO. 209:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

WGGRTLASAV SIPLRKCHSH RPTVLARKQP QSGVPPPYTA IASPDASGIP VINCRVCQSL 60 INLDGKLHQH VVKCTVCNEA TPIKNPPTGK KYVRCPCNCL LICKDTSRRI GCPRPNCRRI120 INLGPVMLIS EGTTSSACIA QSQPEGYKGR VLGHGWGTHS LWDG 164

- (2) INFORMATION ON SEQ ID NO. 210:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SSAVPDGAVG RPVAVAVGGP PHSCRCRPCC LMAAIGVHLG CTSACVAVYK DGRAGVVAND 60 AGDRVTPAVV AYSENEEIVG LAAKQSRIRN ISNTVMKVKQ ILGRSSSDPQ AQKYIAESKC120 LVIEKNGKLR YEIDTGEETK FVNPEDVARL IFSKMKETAH SVLGSDANDV VITVPFDFGE180 KQKNALGEAA RAAGFNVLRL IHEPSAALLA YGVGQDSP

- (2) INFORMATION ON SEQ ID NO. 211:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 186 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

RKWTLTSMSQ KRMLKRPDNK LKYVTKWQRT AKQITHPFSR NSTMSSMNIT ILTSPTSSRK 60 YKRAEERRIV RMGESMKTYA EVDRQVIPII GKCLDGIVKA AESIDQKNDS QLVIEAYKSG120 FEPPGDIEFE DYTQPMKRTV SDNSLSNSRG EGKPDLKFGG KSKGKLWPFI KKNKLMSLLT180 GGPFSF

- (2) INFORMATION ON SEQ ID NO. 212:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN

- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ISGRRVSLNF VSEFSITEFC PCWCLGYRPD GPGSFPSCSG LEVSPLHFLK ACVQCSPKSI60

- (2) INFORMATION ON SEQ ID NO. 213:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

DLCSTLSATK GSITCFLNKA LVSPPASSGL HYSETNSTSF AGGITVPISR LGPALQTSFG60 LLVLLTLL

- (2) INFORMATION ON SEQ ID NO. 214:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

(2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LPTAFLLSSV FWIFMTWFIL FFPDLAGAPF YFSFIFSIVA FLYFFYKTWA TDPGFTKASE 60 EEKKVNIITL AETGSLDFRT FCTSCLIRKP LRSLHCHVCN CCVARYDQHC LWTGRCIGFG120 NHHYYIFFLF FLSMVCGWII YGSFIYLSSH CATTFKEDGL WTYLNQIVAC SPWVLYILML180 ATFHFSWSTF LLLNQLFQIA FLGLTSHERI SLQKQSKHMK QTLSLRKTPY NLGFMQNLAD240 FFQCGCFGLV KPCVVDWTSQ YTMVFHPARE KVLRSV

- (2) INFORMATION ON SEQ ID NO. 216:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

SPSRSPVVFA GEFLFKHPFV EESLMSFFHP DLHLMNPKAI STQFLYSVF

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- (2) INFORMATION ON SEQ ID NO. 217:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217: KEINNYIRKE KNFKYLQPST PNHPQDRWVQ KNAPWFY 37 (2) INFORMATION ON SEQ ID NO. 218: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 52 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218: KFSSKDDRTS RRRSIIISER KKILSIYNPL LLITPKIGGS RKMHLGFTEE RS 52 (2) INFORMATION ON SEQ ID NO. 219: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 150 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

- (2) INFORMATION ON SEQ ID NO. 220:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

NKWNKSKLGK EISKATQSLD PAQLADPCHS LAVAASLCSL KGEPGQCFPS PWAWSLHSGK60 QTSGPFPKSQ ECLAAWWVLI AMF 83

- (2) INFORMATION ON SEQ ID NO. 221:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

NSKLVDCRME TWLLRHWVSF SLCVSCWGVV MIVSALTHCT RWQQDTALHK MAAPLQLPPQ60 PPSLHPHRFG LWFLSSVTYC LRS 83

- (2) INFORMATION ON SEQ ID NO. 222:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CLHNREPDIF RILSSSYYGI LRPRSYLQTK WPWSLQNIAM STHQAARHSW DLGKGPLVCF60 PLCSDQAQGL GKHWPGSPFS EHREAATARE 90

- (2) INFORMATION ON SEQ ID NO. 223:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

QSLRHCWLNI SLQRDGAFKE PGAGPVSSKA LDVFLVRTRR GCQMPLKPSG LVWPRAAGQG 60 RAEKWSSSQL ALPSPTQPRP RWSLDSILTS ASPKVQMSKC LVVQSQEMGS YLKS 114

- (2) INFORMATION ON SEQ ID NO. 224:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GCVGGGRAEA MAEKFDHLEE HLEKFVENIR QLGIIVSDFQ PSSQAGLNQK LNFIVTGLQD 60 IDKCRQQLHD ITVPLEVFEY IDQGRNPQLY TKECLERALA KNEQVKGKID TMKKFKSLLI120 QELSKVFPED MAKYRSIRGE DHPPS

(2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GQTMRTEGLR GVSRAQSHLS RKVASALAVP ASRRIAVPGD LHTGRVSWLR RRVILPPDAS60 ILSHVFRKYF RKFLNQQAFK FLHGVDLAFN LLIFS 95

- (2) INFORMATION ON SEQ ID NO. 226:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ALRPPLYALG QQVGAVTGPA DCSATAPLDF WIFWKQSQNS GLLGGWQRGM VRGPPFISLF60 SIRWQSTGHP WWVSGPRPMP TLPFESR 87

- (2) INFORMATION ON SEQ ID NO. 227:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

APALATQPPL SLPRGTGPAY LNSLTLMLQT WLLDSKLLSS NVLLPHFHFL HICLLLYWFL60 LLNLYFHSWV LCLPPFFSA 79

- (2) INFORMATION ON SEQ ID NO. 228:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

RSMSVEASFV CLGTTGRCCH WSCRLFSNSP FGFLDILETK SEQWPTGGLA EGYGKRTSFH60 LPVQHPMAVH RSSLVGVRPK THAHLTL 87

- (2) INFORMATION ON SEQ ID NO. 229:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATLSRFFGRI FNLRLTQVFP FLFSSPNDKK SFCSIEGEWN GVMYAKYATG ENTVFVDTKK 60 LPIIKKKVRK LEDQNEYESR SLWKDVTFNL KIRDIDAATE AKHRLEERQR AEARERKEKE120 IQWETRLFHE DGECWVYDEP LLKRLGAAKH

(2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

DSLRRGLGIC LWEFIHLSLL FTSPKPGFPL LKPAVISQLE GGSELGGSSP LAAGTGLQGS 60 QTDIQTDNDL TKEMYEGKEN VSFELQRDFS QETDFSEASL LEKQQEVHSA GNIKKEKSNT120 IDGTVKDETS PVEECFFSQS SNSYQCHTIT GEQPSGCTGL GKSISFDTKL VKHEIINSEE180 RPFKCEELVE PFRCDSQLIQ PSREQH

- (2) INFORMATION ON SEQ ID NO. 237:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

RIRRSALIFS KGVQRWRRVF GRRVSPGSGN TESEASDYRK KQGTSKVFGR RVLKKIQ 5

- (2) INFORMATION ON SEQ ID NO. 238:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

GTLFFTVVTG FALCVPAAGT YPPSENPPPS LYTLGKDQCR TPDP

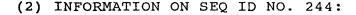
44

- (2) INFORMATION ON SEQ ID NO. 239:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

NLYPTLEFNP SHFVVELTGF FSTPFFRTPL RYLVFYGSHW LRSLCSRCRD LPAFRKPAA160 SVHPWKRSVQ NAGS 74

- (2) INFORMATION ON SEQ ID NO. 243:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 183 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

AAVAFGAKGT SPAEARSSRG IEEAGPRAHG RAGREPERRR SRQQRRGGLQ ARRSTLLKTC 60 ARARATAPGA MKMVAPWTRF YSNSCCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP120 DQYNFSSSEL GGDFEFMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAG SSHSSVTRSL180 TLP



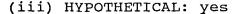
- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

CQHVHCHCDF SSHDPDMCYG YLRSVQATRS WIIPFFCYQI FDFALNMLVA ITVLIYPNSI 60 QEYIRQLPPN FPYRDDVMSV NPTCLVLIIL LFISIILTFK GYLISCVWNC YRYINGRNSS120 DVLVYVTSND TTVLLPPYDD ATVNGAAKEP PPPYVSA

- (2) INFORMATION ON SEQ ID NO. 251:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

ATKTVPRQRW SPPHCPRPNP SLNLLRCGWG NRGKTEAPDA FSLLCSSAID CPDVQRETHT60 RFAHENWGAD GQADRLCLFS E 81

- (2) INFORMATION ON SEQ ID NO. 252:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF



- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GVDGETEAKL RHLMHSACCA AVPLTALMFR EKRTQGLPMR IGEQMAKQIG YVCFLSDEVR60 KPCGSGGHLW FILFPYPWLL EMVTFRTVQL HLSEHYC 97

(2) INFORMATION ON SEQ ID NO. 253:

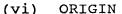
- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

LEILGIFSRV SKLSSSPTDT HPSSQIGVAI LGGRVVYGTP GCLHISQNYP RTIVPKSRVF 60 TGRQNLFSMP VPQLLSQIPI LGSHQLPIPH QTATVPSLSP YCSFKSCSQE RNCH 114

- (2) INFORMATION ON SEQ ID NO. 254:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

(2)	INFORMATION ON SEQ ID NO. 255:	
	 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 35 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: ORF	
	(iii) HYPOTHETICAL: yes	
	(vi) ORIGIN (A) ORGANISM: HUMAN	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:	
	QVDTLISTRK GLKLQNQCSL DSQTNDFSTV TPGID	35
(2)	INFORMATION ON SEQ ID NO. 256:	
	 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 41 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: ORF	
	(iii) HYPOTHETICAL: yes	
	(vi) ORIGIN (A) ORGANISM: HUMAN	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:	
	TKPQRHRTTM GKGHFLGSEY DLQNGPCGLC IYPYAVPWSN A	41
(2)) INFORMATION ON SEQ ID NO. 260:	
	 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 205 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: ORF	

(iii) HYPOTHETICAL: yes



(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GSVKVPASPR PGGTSLLGPV AAKELSFSRP NGRRGQLPRP PGSLTLLLFF SSPASRGPAS 60 LSPGGIRLL PPPPHLLPGQ PACPAAVMCD KEFMWALKNG DLDEVKDYVA KGEDVNRTLE120 GGRKPLHYAA DCGQLEILEF LLLKGADINA PDKHHITPLL SAVYEGHVSC VKLLLSKGAD180 KTVKGPDGLT AFEATDNQAI KALLQ 205

(2) INFORMATION ON SEQ ID NO. 264:

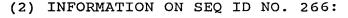
- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

RNMSSFSRAP QQWATFARIW YLLDGKMQPP GKLAAMASIR LQGLHKPVYH ALSDCGDHVV 60 IMNTRHIAFS GNKWEQKVYS SHTGYPGGFR QVTAAQLHLR DPVAIVKLAI YGMLPKNLHR120 RTMMERLHLF PDEYIPEDIL KNLVEELPQP RKIPKRLDEY TQEEIDAFPR LWTPPEDYRL180

(2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

VIGYPSRINS EPSPVIYNRP GNNVKLNCMA MGISKADITW ELTDKSHLKA GVQARLYGNR60 FLQPQGSMTH SACHKEGW 78



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

ATPLCGMLNG SLIPGVEEIC FHTDEPEPLP SDATYPLTPT

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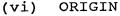
(2) INFORMATION ON SEQ ID NO. 267:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

VGIWQEDHLP QSLGFLNKKE IVFLSWLLRL LKLALPLKYD ISFAVLNLKL VASSVAHFQF 60 LYQASLLSFP LRMGQVCSGG HSVRFSRGFG RGFKGKYSGG RMGSGVKVGD KGGRAKGGVE120 GWGPYLDRGM PGGQGK

(2) INFORMATION ON SEQ ID NO. 268:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes



(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

LVYPKQGTKE PGKRSGHVKR DTQDTLRDQS GSTPVLLPEC LCVNPCFLQN KRQQRKLLNQ60 NTDPMRNGAC FCDPGELSAR LQELTDGQLL IF 92

(2) INFORMATION ON SEQ ID NO. 269:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

NLVYTMWLQI YVNVHFEHIY VLWKEMLVTK IRFTLKEEEF YSKHSNILFK CFKIQSIVFK 60 VAVKASTYVK TQKEGSSDKN TAPLLCCFSC SLYTLSKHLL SGA 103

(2) INFORMATION ON SEQ ID NO. 270:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

FIYKQSKVRD IFAVTLAILS LQSPTSRVQC TSNNSLKTRH LTISVYLVCK VNKKSSIIKE60 LCFYQRSLPS EFLHKLMPSL QL 82 🚅

(2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

QQHHLPQSLG FLNKKEVVFL TWLLRLLKLA LPLKYDISFA VLNLKLVASS VPHFQFLYQA60 SLLSFPIRMD MCCSACHVCN ASCREFGHSI KEKIQ 95

- (2) INFORMATION ON SEQ ID NO. 275:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

LLHQYHTSSF YTKPVSSVFP LEWTCAVQRV MSVMLHAESL VIVLKRKYSE VTMSPE 56

- (2) INFORMATION ON SEQ ID NO. 276:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

HAEQHMSILM GKLRRLAWYR NWKCGTDEAT NFKFRTAKLM SYFKGRANFN NLNNQVKNTT60 SFLLRNPND

- (2) INFORMATION ON SEQ ID NO. 277:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - ORIGIN (vi)
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

YILEISPLKP SLAPTSCGLM PQGFPPHFCN PRYPSLSTPS QTPTPGIARE DFGLANCVGY60 VSVVLIRDVH DCQSAFLTSV TTLLRCNSSQ KKTFS

- (2) INFORMATION ON SEQ ID NO. 278:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 133 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

PTQFARPKSS RAIPGVGVWD GVDNEGYLGL QKWGGNPWGI SPQEVGASDG FRGDISNIYQ 60 PWALSPCCSQ HGPHTSSLRL TWELVRNAGS PRSIELEAVL TRSPVIFMAQ SSFLRDRCRL120 133 LSAGMRHPWG RCG

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LKQHSHNQHN LLGQSLHGQS LGWESGMGWI MKDTWGCRSG VGIPGASVHR RWGPAMASGV 60 IFPIYISPGH SRPAAHSMVL TPAASALPGS LLEMQDLPDL LS 102

- (2) INFORMATION ON SEQ ID NO. 283:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

VYSANEGQNF QFIDGYSAAD ESLCVSHFNF CKQRHRPRTV RGRTSFSSKL PRHNKENSTF60 ISRKPMECSN EEVVNQGQSD GSMGKF 86

- (2) INFORMATION ON SEQ ID NO. 284:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

GAELVFLQNC LGIIRKIALL FQGNRWNVQM RKLLIKGSRM DQWVNFRWRQ GGAYIHSNPD60 VIWSGQGWK

- (2) INFORMATION ON SEQ ID NO. 285:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

LTTSSFEHSI GFLEIKVLFS LLCLGNFEEK LVLPLTVLGL CLCLQKLKWL THKLSSAAE 59

- (2) INFORMATION ON SEQ ID NO. 286:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

GKEPQPESNS IMVKFPTESS CEWVIRKNED PKDKNQRQMG SVTGSLSSIL NPIEYCGLTK60 CQGGD

(2) INFORMATION ON SEQ ID NO. 287:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 48 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:	
FLSFGSSFFL ITHSQDDSVG NLTMIELLSG WGSFPHRKDI LKTKKYLN	4
(2) INFORMATION ON SEQ ID NO. 288:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 32 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:	
ARNIQSDLEW MIKIQSQTPS VFDFCLLDPH FS	32
(2) INFORMATION ON SEQ ID NO. 292:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 76 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CAKLETGFDF LSYLFAFCAS PSNLVHLSSH SCYFQVKQDI LGVKSLWVFC FYVYKNGFCV60 PFPCKYQLIW KLTIIM 76

- (2) INFORMATION ON SEQ ID NO. 293:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

VELSLLFPQL SQLLVNFKEA GHDDSHLLSQ NFGRRRWADS LSPGVQDEPG QYGPTSSLTK60 HPH 63

- (2) INFORMATION ON SEQ ID NO. 294:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

PPKCLVSLEN NMNETKDEPD YLVTHRRRTS SSGNQILFQA WHIKGKKGSE RRVRKYHLKP60 QKIWQKTASK SIR 73

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

PLGPASSAFG PSGSKSRSEE GRDGTASPGT FKYHPWSPLS SLREWTSQST SSGLSDLLLC 60 LYQPWQGSRI HLVGSGPSQY HWGSNKFLEP QSLGPGSQLI GDGVPFQARA EFGTSGHELE120 GNSVSYELGP WP 132

- (2) INFORMATION ON SEQ ID NO. 299:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

ESRRGALAGP LSKAGEGRPG WYLNVPGMLS HPFLPHSYSL TLMAKARDAG PKGKNVLSVF60 SGFYSLVSLH 70

- (2) INFORMATION ON SEQ ID NO. 300:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

GVKAREYRED VFTFRACVSG FGHQGQRVGV RKEGMGQHPW DVQVPSWSPF SSLREWTSQS 60°-TSSGLSDLLL CLYQPWQGSR IHLVGSGPSQ YHWGSNKFLE PQSLGPGSQL IADGVPFKLV120 PARAEFGTSL KGNSVTYELG PWP 143

(2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 408 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

FANWEFMGTE QLQPQLPSPK VWSCRGCRQG PTKFNQVSRM QTPAPVSRRV GLAVSLTPPP 60 SGQSGPSVMG KAAACPATPA SAPSQGLSFG GPVSCWPGSP LLHLIGGRQL LDLCPGCGRS120 LPFSSSSSS VSNDSAPDGP RGLGCFGGVV LGGRGFKYLL YFLFVAATQQ ILLLGRASAF180

LKRDVGDPLV VAPAFFAVAG HLHQAVALPG VRVRVRDQET MQVSGLGGAL GLGRLSQELR240 QALHARHPHD VDVVVTAEGL DEREVDLQGD VILLLLVNGQ EAEDHAVWVH IHQLGRLVHP300 HCEAILALSG HQKLLHRGGH RLHLLRRVVA RHELFQRHVA IIIHSGCGST AVPREKLQNP360 SQRAQNLPTE LERSSKTFGK QRNPSRKGGK IYCKVLGEDN PGSCGNQR 408

- (2) INFORMATION ON SEQ ID NO. 305:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GWGVWQAGLD PVLGPPSSAV PSLLLGVVSM VWPHLQLCLS AVPLASSSLN SAAWSPVSSR 60 ARQGWGGWCW QQLLSWCDLS GLHLRGRNGP GYRGQIHPGW SPRPPGLGAA GGRWLLVGRW120 PSCLACLPCL SSSPNALSVS AFLAPGLSTP SAYKAVSPPQ TTVWLQPIR 169

- (2) INFORMATION ON SEQ ID NO. 306:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ILQLGHQFPL VPARAGAVGV GSSFSLGATF PASTSEVGMG QAIEVRFIQA GVLVLRAWGL 60 LGGAGCWWEG GHRAWLVFPA SLLLLTLCLS LLSWPRASPL PQLIRLCLLL RPQSGSSPSG120

- (2) INFORMATION ON SEQ ID NO. 307:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 472 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

SESLTHPGEE PGGPPPGGAP TMATPLVAGP AALRFAAAAS WQVVRGRCVE HFPRVLEFLR 60 SLRAVAPGLV RYRHHERLCM GLKAKVVVEL ILQGRPWAQV LKALNHHFPE SGPIVRDPKA120 TKQDLRKILE AQETFYQQVK QLSEAPVDLA SKLQELEQEY GEPFLAAMEK LLFEYLCQLE180 KALPTPQAQQ LQDVLSWMQP GVSITSSLAW RQYGVDMGWL LPECSVTDSV NLAEPMEQNP240 PQQQRLALHN PLPKAKPGTH LPQGPSSRTH PEPLAGRHFN LAPLGRRRVQ SQWASTRGGH300 KERPTVMLFP FRNLGSPTQV ISKPESKEEH AIYTADLAMG TRAASTGKSK SPCQTLGGRA360 LKENPVDLPA TEQKENCLDC YMDPLRLSLL PPRARKPVCP PSLCSSVITI GDLVLDSDEE420 ENGQGEGKES LENYQKTKFD TLIPTLCEYL PPSGHGAIPV SSCDCRDSSR PL

- (2) INFORMATION ON SEQ ID NO. 308:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

PGFALRGAIG PREGRGGGRG YRRSSGRQPL VSWQRQARCG SGGAMSFCSF FGGEVFQNHF 60 EPGVYVCAKC GYELFSSRSK YAHSSPWPAF TETIHADSVA KRPEHNRSEA LKVSCGKCGN120 GLGHEFLNDG PKPGQSRF 138

- (2) INFORMATION ON SEQ ID NO. 309:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

SYGATAAFLS RSEASYFRTD CETGFRFLPS WTRGQGCAPS ACLPSRSQTI PTLAGLEGFD 60 QSGSCSDQGQ GGWQGRPPFP FCLLSSLGDV GLSFGEDESL SWNWASQGRV QRQGQEKKVR120 V

(2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 249 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

SEQGAKSADS VAAQPRPVPA EGMNHQQMSL FSKKRKGLVQ SRGLGSVLMF QPLRPAFLSR 64
RPGFQLQGGM ANVWPQCGGR LGWVWAARLV TLGGRSFFAF RDKLQRAAEY SESGLPRLGA120
VVQELVAQPI ATLATGHLQG FRSIVLRTLG HAVGVNGLGE RRPWRRVCIL RAAGEQLIAT180
LGTHVNARFK VILENLAPEE AAERHGATGT AARLPLPTDQ RLPTRRPPVP ASTSPPLPRT240
NRSPEGESR 249

- (2) INFORMATION ON SEQ ID NO. 311:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

LGSSWIFVNL TVRFCILGKE SFYDTFHTVA DMMYFCQMLA VVETINAAIG VTTSPVLPSL 60

IQLLGRNFIL FIIFGTMEEM QNKAVVFFVF YLWSAIEIFR YSFYMLTCID MDWKVLTWLR120 YTLWIPLYPL GCLAEAVSVI QSIPIFNETG RFSFTLPYPV KIKVRFSFFL QIYLIMIFLG180 LYINFRHLYK QRRRRYGQKK KKIH

- (2) INFORMATION ON SEQ ID NO. 312:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

RISGCSPRSS CCFQCPTADR FKKPTEQQQN EVFLRSIQKC TVPPLTRTST QVNGLSQCRR 60 WKAAIFYVCA QPYSLEVCLA YSNISSLSKA VHCYCQFDLH TVFPLDPCYH LDLVCVCVYV120 CLCVCGLVWF ETGSCTVTPG CSAVAQSRLT AALTS

(2) INFORMATION ON SEQ ID NO. 313:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AVMDQVMQFV EPSRQFVKDS IRLVKRCTKP DRKEFQKIAM ATAIGFAIMG FIGFFVKLIH60 IPINNIIVGG

- (2) INFORMATION ON SEQ ID NO. 314:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - ORIGIN (vi)
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

FRNRKHLERK KKNPQNIQAN LYSVSFSHPH TCSPISKMKN SLPKCIQPPT MMLLIGIWIN 60 FTKKPMNPII ANPIAVAMAI FWNSFLSGLV HLLTSRMESF TNCRLGSTNC IT 112

- (2) INFORMATION ON SEQ ID NO. 315:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

DEKLSSKMYS ATNNDVINRN MDQFHKEANE SHYSKSYCCC HGNLLEFFSI RFSASFNQPN 60 GVLYKLPTWL NKLHYLIHDC LPNRHLKCQG HVALELADGG PPEPESGFLP 110

- (2) INFORMATION ON SEQ ID NO. 316:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

GSSEGSYSSQ TETCPLTPSL VTGSMFAQNF LRGLSLQKSN LLPECCLASE NLTLSFPSVN 60 GHRCVAQGSE TSESRAQWHG VALVVRKVIG QLYCKRNKYV VQFCKCQVCS VVL 113 (2) INFORMATION ON SEQ ID NO. 317:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

GKRGQLWSLN LLAPCAGYKT RSWSKIALTP NPNAVQDLGA TQPVVIWCWF PFFVCLLVSK 60 IALLGTAWKV QAFLLARSGL ASSPCLHSVP KEDFCSTLWS 100

- (2) INFORMATION ON SEQ ID NO. 318:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

SQIISNLVDN YSIQELMFSE TVINRIFTSG LAGRLGGRKG RVEGWVAHQN GDEPGKTTML 60 LFLYPLKPIS RVLNDAFFVC FLIGSQISFS IKNWGYKPKE T 101

- (2) INFORMATION ON SEQ ID NO. 319:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

WWRLNNKSAK VRQQAADLIS RTAVVMKTCQ EEKLMGHLGV VLYEYLGEEY PEVLGSILGA 60 LKAIVNVIGM HKMTPPIKDL LPRLTPILKN RHEKVQENCI DLVGRIADRG AEYVSAREWM120 RICFELLELL KAHKKAIRRA TVNTFGYIAK AIGPHDVLAT LLNNLKVQER QNRVCTTVAI180 AIVAETCSPF TVLPALMNEY RVPELNVQNG VLKSLSFLFE YIGEMGKDYI YAVTPLLEDA240 LMDRDLVHRQ TASAVVQHMS LGVYGFGCED SLNHLLNYVW PNVFETSPHV IQAVMGALEG300 LRVAIGPCRM LQYCLQGLFH PARKVRDVYW KIYNSIYIGS QDALIAHYPR IYNDDKNHLI360 IRLMNLGL

- (2) INFORMATION ON SEQ ID NO. 320:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

YPFFTLCQRN RVFDISSYVK EMLQNVNCFK LKLPLKRPRY IYLIVYIMFN ICQSILQVCS 60 FISIKYGYYV AQLLKWYCIV YICTPNNIVC TFCFLYCICA GFFRLYQCNL CLLRYVQKMS120 I

- (2) INFORMATION ON SEQ ID NO. 321:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

FFFFFFFFF HSNVYFFFFF FFFFFGKNVI YLHCFHSSTV VLGLNISITL LFPIYILLEY 60 YYKYNIQFKK TYGETQLMFF SPLYRLLSII RLQWKFIWTF SVHILKGRDY TDKA 114

- (2) INFORMATION ON SEQ ID NO. 322:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 597 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

EKCGQYIQKG YSKLKIYNCE LENVAEFEGL TDFSDTFKLY RGKSDENEDP SVVGEFKGSF 60 RIYPLPDDPS VPAPPRQFRE LPDSVPQECT VRIYIVRGLE LQPQDNNGLC DPYIKITLGK120 KVIEDRDHYI PNTLNPVFGR MYELSCYLPQ EKDLKISVYD YDTFTRDEKV GETIIDLENR180 FLSRFGSHCG IPEEYCVSGV NTWRDQLRPT QLLQNVARFK GFPQPILSED GSRIRYGGRD24QC YSLDEFEANK ILHQHLGAPE ERLALHILRT QGLVPEHVET RTLHSTFQPN ISQGKLQMWV300 DVFPKSLGPP GPPFNITPRK AKKYYLRVII WNTKDVILDE KSITGEEMSD IYVKGWIPGN360 EENKQKTDVH YRSLDGEGNF NWRFVFPFDY LPAEQLCIVA KKEHFWSIDQ TEFRIPPRLI420 IQIWDNDKFS LDDYLGFLEL DLRHTIIPAK SPEKCRLDMI PDLKAMNPLK AKTASLFEQK480 SMKGWWPCYA EKDGARVMAG KVEMTLEILN EKEADERPAG KGRDEPNMNP KLDLPNRPET540 SFLWFTNPCK TMKFIVWRRF KWVIIGLLFL LILLLFVAVL LYSLPNYLSM KIVKPNV 597

- (2) INFORMATION ON SEQ ID NO. 323:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

IRRDKAYLTF KWRDDENPLI QSFRTKRQSS DKSMTWMKCP TGALDIFNFC DYVKEVDFTD60

NGAEANISKR NPNFFP 76

- (2) INFORMATION ON SEQ ID NO. 324:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

FFLYSFSSDN HDFRSFKTIY LAFVSGGELA ISILKPAIIV NLRTGLSWGS EGKELFEQMC60 VGGTGFHPTA KLVLLEISFY NTKISLCQRF 90

- (2) INFORMATION ON SEQ ID NO. 325:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TRSLLYFHMF LILWEEVGIP FTNVGFCSII CKVHLFHIIA EIKDVQGPCR AFHPCHTLIR60

- (2) INFORMATION ON SEQ ID NO. 326:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 42 amino acids

(B) TYPE: Protein(C) STRAND: individual(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:
IRNEKKGCVL SVGEMELVLV VLEQDRHLVL MLWSFVIVEH RG 42
(2) INFORMATION ON SEQ ID NO. 327:
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 50 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:
ATCSDNRSKI FQLFNLECYV LLEPAICMYR INNFYSFGQV ILRQSQWIQK 50-
(2) INFORMATION ON SEQ ID NO. 328:
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 48 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

PKGVVVNPGA LLSQRTTASE LSACPAPTLP GPVPSHLLIR HSLSSHSL

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- (2) INFORMATION ON SEQ ID NO. 329:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

ISEVAVNESV LLLASVCLPI DTHYTNVPSK CSLHICFHCV PTGAMKCVRS PSSGGMSAAL 60 TTAIRIVLCG IFIYINFICT VISLFICQVT ICKSYTHKLL 100

- (2) INFORMATION ON SEQ ID NO. 330:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

EAQKWDCIWT KNYKKVQSLV SRMQALALGD GSSLENAAAD SLFQRRSFER RVCYISFTV 60 TLWRLKDLVV SCFLKITGIW RPVKPFWTDI SSKYFFIKVF EGDDFLDLWL DILGFPDYIV120 LS (2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

ENWASRYFQS SFTEQKVWVG HWLEGDSPTL TVTIWAATGG IVQLASRCIP HLKYCWIKAI 60 YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLFH SWFFFFFFLQ DLAVTQDGVQ120 WHDH

- (2) INFORMATION ON SEQ ID NO. 332:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LNVDLLITRR LCEKIYVYIY MICRSHFFYQ ALFSLQSHSL TVCNSWFMLM IDKYPVFVTF60 SNYHCNDNLS HVYTCNFLAS FP 82

- (2) INFORMATION ON SEQ ID NO. 333:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF



- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

RLVKYKNSLN REKASQVFPL KVKYGTFHFN KVNDFKNLTF FRRKKKTSYE PSLVNHLVYK60 IFPLFKKCFC KILRSHEIMP WS 82

- (2) INFORMATION ON SEQ ID NO. 334:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

KLEYIMSTAN CSFCLILTDY AFPQRSSRSH IYRHIYGSGL KEKTILSSIM IYHCAINQKN60 QVRNTIKTTL KGKNF 75

- (2) INFORMATION ON SEQ ID NO. 335:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

NEYCSWSTCI KQKTCQLLGA NTQNLVPVFF FFLTTIVYTF LKIKFVTKSP MSFTCIYDHQ60 MVIRATYVNA CL 72 (2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

THNTSTITAY RKLQSTLQAS KVHSVAQSPW RGRDLKVLMS SYFTCFLLST QCKMNFLHSL60 YFRLKIDSFL VLTLTLEGTV VPGKRSRFTV PNH 93

- (2) INFORMATION ON SEQ ID NO. 337:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

LGPRGEIEVY LAKSLAEKLY LCQYPVRPAS MTYDDIPHLS AKIKPKQQKV ELEMAIDTLN60 PNYCRSKGEQ IALNVDGACA DETSTYSSKL MDKQTFCSS 99

- (2) INFORMATION ON SEQ ID NO. 338:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GKSRRSACPS ASRNTCWSRR RRPRPRSAQS APLCCGNSWG SGCRWPSQAL PSAAWA

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- (2) INFORMATION ON SEQ ID NO. 339:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

GRAEGLLVHQ LRGIRAGLVG AGPVHVQRNL LPFAAAIVGV QGVDGHLKLY LLLLGLDLG 59

- (2) INFORMATION ON SEQ ID NO. 340:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

QPSSLLHHCP YPYPPRHLLA TPLLKPQLLA GSPAHASLIS FLASPQRASR QHGGPSQRAG 60 TLSCPLVELG GSSGGRGLCH GSADPTNRAA EPQERGEPAA GDRRPLPEWG RVSLAESPGA120 EFRCPGSLGE WGEIPEKESS AHPKTEEAAL CPAPGSH

(2) INFORMATION ON SEQ ID NO. 341:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 260 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

NHSCWQGPQL MPASSPELLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT 60 QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRAVLTQK120 QKKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA QGYGVRIQDA GVYLLYSQVL180 FQDVTFTMGQ VVSREGQGRQ ETLFRCIRSM PSHPDRAYNS CYSAGVFHLH QGDILSVIIP240 RARAKLNLSP HGTFLGFVKL

- (2) INFORMATION ON SEQ ID NO. 342:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TPASWIRTPY PWACRPLPRL RAGCHITSVT SESSLEVALM GTRCRTECCF FCFWVSTALL 60 FRDLSPLSQA SRASELCSGR LCQGYPSPFW EGPPVPCSRL TSLLRLCSSV CWVSRAMAQA120 TAPRAAPQLN QRATESAGSL TGPPMLPGGP LGASKKGDEA GMSWGPCQQL WFQEWGSKEV180 AGRVRVRAVV QKGRRLLRKE K

- (2) INFORMATION ON SEQ ID NO. 343:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 165 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GRRSRMEIPV PVQPSWLRRA SAPLPGLSAP GRLFDQRFGE GLLEAELAAL CPTTLAPYYL 60 RAPSVALPVA QVPTDPGHFS VLLDVKHFSP EEIAVKVVGE HVEVHARHEE RPDEHGFVAR120 EFHRRYRLPP GVDPAAVTSA LSPEGVLSIQ AAPASAQAPP PAAAK 165

- (2) INFORMATION ON SEQ ID NO. 344:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TALAQPQASQ AQSPHPPNVL DCTDLPLQTI QAWFPRPDPS PATRQSTTAP SSPFSAVKPQ 60 PATPDSGTLF RLPQLLDTRP TRTPNTKLYR LSHPNLPRLC TDVLGPLPNS NQTPSP 116

- (2) INFORMATION ON SEQ ID NO. 345:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

DIRAESGEVG VGESVQFGVG CSSWPGVQEL GQSKKGSRVW CGWLGFHGRK WAGGGSC GCRGRIGSWE PGLDGLEWEV CAVQDVWGVG GLCLTGLGLG QGCLHHNLVS K	RLS 60 111
(2) INFORMATION ON SEQ ID NO. 346:	
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 53 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:	
RTEEEKKKKE KNQQPQLPTP KCWSFYVKGR IPGYGHGVYK YVGRFSANSF PTV	53
(2) INFORMATION ON SEQ ID NO. 347:	. "
 (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 51 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:	
NEI MENDAE I SUCMOSHKO AFPASHOINE USMSIOIDI E EKNNHAFIND N	51

(2) INFORMATION ON SEQ ID NO. 348:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLLDFVL VLALFLIFFY 60 YESPGRRGDS GSWPGPGRQV ALEMGKCLCR GAELSLCFSF FPLLLPLHTP VAGRNLGFPE120 SLGVPPFLPH PGGTPRAPGL FLLLFSFWAV

(2) INFORMATION ON SEQ ID NO. 349:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- MOLECULE TYPE: ORF (ii)
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

RSFLTRSVIK LPKRKTRGET SPGPWAFLPG GVRRVGPPSF QGSRGSFQPR GCEGEGVEEK 60 RRNRERAQRL DTDTFPSPGP PAVLAQASSH CHLCVQEIHN KKKSKTKPKP KQNPKGKDLG120 QWNEEEGRRG R

(2) INFORMATION ON SEQ ID NO. 350:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 151 amino acids

 - (B) TYPE: Protein (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

RKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNKIQKEK 60 TWGNGMRKRG GEEGRRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVFG GRLPIHPVEI120 LVAGLLGGVK PVSDRQAGKG LGDGGCGRER V

- (2) INFORMATION ON SEQ ID NO. 351:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

TLTAHEGRGG KCTEEGDASQ QEGCTLGSDP ICLSESQVSE EQEEMGGQSS AAQATASVNA 60 EEIKVARIHE CQWVVEDAPN PDVLLSHKDD VKEGEGGQES FPELPSEE 108

- (2) INFORMATION ON SEQ ID NO. 352:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

(2) INFORMATION ON SEQ ID NO. 353:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TYSIHLHSQT KLKSLKVHKK IAQLKSAEYT QNCHPTVFSV FPAILFPPQT SSAPSHPKYA 60 IVFVILIKIL KQKFIVEQFM STKVCLSCSC PVCISSGFII QIKKILKNFL VTACMQPLSV120 PL

- (2) INFORMATION ON SEQ ID NO. 354:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 457 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

PVCEPLSCGS PPSVANAVAT GEAHTYESEV KLRCLEGYTM DTDTDTFTCQ KDGRWFPERI 60 SCSPKKCPLP ENITHILVHG DDFSVNRQVS VSCAEGYTFE GVNISVCQLD GTWEPPFSDE120 SCSPVSCGKP ESPEHGFVVG SKYTFESTII YQCEPGYELE GNRERVCQEN RQWSGGVAIC180 KETRCETPLE FLNGKADIEN RTTGPNVVYS CNRGYSLEGP SEAHCTENGT WSHPVPLCKP240 NPCPVPFVIP ENALLSEKEF YVDQNVSIKC REGFLLQGHG IITCNPDETW TQTSAKCEKI300 SCGPPAHVEN AIARGVHYQY GDMITYSCYS GYMLEGFLRS VCLENGTWTS PPICRAVCRF360 PCQNGGICQR PNACSCPEGW MGRLCEEPIC ILPCLNGGRC VAPYQCDCPP GWTGSRCHTA420 VCQSPCLNGG KCVRPNRCHC LSSWTGHNCS RKRRTGF

- (2) INFORMATION ON SEQ ID NO. 355:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

GVRAASKEIE ELRRAHREGT SRAVTGEGPA AGRMTVPKQT QTPDLLPEAL EAQVLPRFQP 60 RVLQVQAQVQ SQTQPRIPST DTQVQPKLQK QAQTQTSPEH LVLQQKQVQP QLQQEAEPQK120 QVQPQVQPQA HSQGPRQVQL QQEAEPLKQV QPQVQPQAHF TAPRAGAAAA EEAGPDTDFS180 TGAHTGHSQA SRHRELLPGA VFSFRPPGAG

(2) INFORMATION ON SEQ ID NO. 356:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 292 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GRAGRRATMF SQQQQQQLQQ QQQLQQQLQQ QQLQQQLQQ QQLLQLQQLL QQSPPQARCH 60 GVSGGPPQQP QQPLLNLQGT NSASLLNGSM RQRALLLQQL QGLDQFAMPP ATYDTAGLTM120 PTATLGNLRG YGMASPGLAA PSLTPPQLAT PNLQQFFPQA TRQSLLGPPP VGVPMNPSQF180 NLSGRNPQKQ ARTSSSTTPN RKDSSSQTMP VEDKSDPPEG SEEAAEPRMD TPEDQDLPPC240 PEDIAKEKRT PAPEPEPCEA SELPAKRLRS SEEPTEKEPP GQLQVKAQPQ AG 292

- (2) INFORMATION ON SEQ ID NO. 357:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

PRRLPSVAVG MVRPAVSYVA GGIANWSSPC NCCKSKALCR MEPLRREAEL VPWRFRSGCC 60 GCCGGPPLTP WQRACGGDCW SSCWSCSNCC CCNCCCWSCC CCNCWSCCCC CWSCCCCCWL120 NMVARLPARP QRSSRPHGWA GPAAPTPRPG GSGPRAPGLP AATPGPVGS 169

- (2) INFORMATION ON SEQ ID NO. 358:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

ISKTKKYCGS PSSRIRLEGG HLEMRKARGG DHVPVSHEQP RGGEDAAAQE PRQRPEPELG 60 LKRAVPGGQR PDNAKPNRDL KLQAGSDLRR RRRDLGPHAE GQLAPRDGVI IGLNPLPDVQ120 VNDLRGALDA QLRQAAGGAL QVVHSRQLRQ APGPPEES 158

- (2) INFORMATION ON SEQ ID NO. 359:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

QSLRTLNLKN KKVLWISLEP NSARGRSPGD EKGPRGGPCA CVPRAAERRG GRCCPGAQAE 60 ARARAGAQTS CPGGPEAGQC QAQPGPETAG WLRPPEATAG PWPSCRGSAG PEGWGHHWP 119

(2) INFORMATION ON SEQ ID NO. 360:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

PPEFGWDAAE TDLLLAEEGS GWRGPHGQQV LGLLWRPRRL SKLPAVDHLQ SSPRSLAELG 60 IQGATEVVHL DIRQGVKAND DPIPRGQLTL CMRAKVPPSP PEVGASLQFQ VPVGLGIVRP120 LAPRDSSFEP QLWLWPLPGL LGSSVLPASR LLVGHRHMVP PAGLSHLQVT ALEPNSARGR180 STVLFCF

- (2) INFORMATION ON SEQ ID NO. 361:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

STIILGKSRI EFFSRCPTRV GQGPQSRLIN SHRIQTPGKI ALRSQLLSSL YGSRKNSTKM60 TGHPMSVMPM KPHLLEKPLN QNYLFS 86

- (2) INFORMATION ON SEQ ID NO. 362:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

ITKAIVFSFV FSSGYTVEVR ESLILLFGAI IKAMQQPKIK HFGSSQDDMS GDRSCGSHSN60 NLMGPEEKTG VNVLSFYYMQ ELC

- (2) INFORMATION ON SEQ ID NO. 363:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

YKNDRSSYER HANETPSSGE ALESELSFFL MSSDAASFLI FLKTVCFCGM YICTPNYLAL 60 GNHSTTQRQL NKEKFNFKYQ VLSNISQTSD FIKGLPANKV HPKYTGEKAR LLQGPRV 117

- (2) INFORMATION ON SEQ ID NO. 364:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids

 - (B) TYPE: Protein (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

SCRCFYCMPD MPLTREWRTP NSPRMTRRHS HVICIFSYQL QIVALLRLPP VQQEMERKHF60 83 SFLHTTPLDN WKYFWVITIL GYF

(2) INFORMATION ON SEQ ID NO. 365:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

QYGPSRVEVE MSYRIANTLG SFLPRLAQSR QQQQNVEDAM KEMQKPLARY IDDEDLDRML 60 REQEREGDPM ANFIKKNKAK ENKNKKVRPR YSGPAPPPNR FNIWPGYRWD GVDRSNGFEQ120 KRFARLASKK AVEELAYKWS VEDM

- (2) INFORMATION ON SEQ ID NO. 366:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

KPTKHRCCQH PKKYRYLNPN IRSRIFFCGQ NWHSTSCWSV WAPIISTDNC YHWISRCLCP 60 LPQPSHPHSL RKVTYPQHSI CRQVPPLPSC WQAWQSASVQ IHWICPLRPS DIQARY 116

- (2) INFORMATION ON SEQ ID NO. 367:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

SSENPPNTAA VNTPRSTGTS IQTSGLEYSS VVKTGIQQVA GLCGLQLLAQ TTVTTGYLAA 60 YAHYHSPATP TASGKLHILN TPFVGKFLHC LLAGKPGKAL LFKSIGSVHS VPAISRPDIK120 SVGRRCWTTV ARSHFFILVL LGLILLDEVG HRVPLSFLFS

- (2) INFORMATION ON SEQ ID NO. 368:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 227 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

WESMNRWYVK PLETSSSKVK AKTIVMIPDS QKLLRCELES LKSQLQAQTK AFEFLNHSVT 60
MLEKESCLQQ IKIQQLEEVL SPTGRQGEKE EHKWGMEQGR QELYGALTQG LQGLEKTLRD120
SEEMQRARTT RCLQLLAQEI RDSKKFLWEE LELVREEVTF IYQKLQAQED EISENLVNIQ180
KMQKTQVKCR KILTKMKQQG HETAACPETE EIPQEPVAAG RMTSRRN 227

- (2) INFORMATION ON SEQ ID NO. 369:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

FIFSLEGSSG RAVPAAQAGG KGGALLLKGG WERSWSESES ESQEGSGGLR HWCPLWPLRL 60 EALGQAPEHK VRLSMEFCST CTADHISLSS FWRSSFQQPL APAVSLQSPD RRLSHDPAAS120 SWSGFCGISP AFSAFSECSP SSLRSHPPAL GASDR 155

- (2) INFORMATION ON SEQ ID NO. 370:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

DLILLRLELL IDEGHLLPHQ FQLLPQELLA VPDLLGQQLQ AASGAGPLHL LTVTQGLLQP 60 LKALGQGPIQ LLPALLHAPL VLLLLSLAAC GAQHLFKLLN LDLLQAALLL QHGH 114

- (2) INFORMATION ON SEQ ID NO. 371:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TASTLRAVFP RPASESPPLR ARSDAEDLTA AMSSNECFKC GRSGHWAREC PTGGGRGRGM 60 RSRGRGFQFV SSSLPDICYR CGESGHLAKD CDLQEDACYN CGRGGHIAKD CKEPKREREQ120 CCYNCGKPGH LARDCDHADE QKCYSCGEFG HIQKDCTKVK CYRCGETGHV AINCSKTSEV180 NCYRCGESGH LARECTIEAT A

(2) INFORMATION ON SEQ ID NO. 372:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 189 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

LATAVTVDFT CLAAVDGYMT SFTTPIALHF GAVFLNVSEF STRIAFLLIC MVAVTSQMAW 60 FATVVAALLS LSLGLLAVLG NVATSTAVIA GILLKITILG KMTRLTTAIT NIWKRRGNKL120 ETSATASHST TTASTSRTFP GPVARSSTLE ALIAAHGCSQ IFRVGAGPQR RRLGRRPGED180 GSQGRGCLF

- (2) INFORMATION ON SEQ ID NO. 373:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 316 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GGDPVVSSSY RSVGCSEQQK PASSDVVLPA TMSYTGFVQG SETTLQSTYS DTSAQPTCDY 60 GYGTWNSGTN RGYEGYGYGY GYGQDNTTNY GYGMATSHSW EMPSSDTNAN TSASGSASAD120 SVLSRINQRL DMVPHLETDM MQGGVYGSGG ERYDSYESCD SRAVLSERDL YRSGYDYSEL180 DPEMEMAYEG QYDAYRDQFR MRGNDTFGPR AQGWARDARS GRPMAAGYGR MWEDPMGARG240 QCMSGASRLA LPLLPEHHPR VRHVPGACEV GAPSRAASRF GFRVWQWHEA DEGGLGRRGP300 QPICEPRRRR ESRAAF

(2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

IPAALLTGSI RMPPCFLFFF LVRKSAVVPV FPVRPHLHA IAKPENQNGK PPGKAPQPRM 60 PLEHAVLGDD VLGEEGGQAE RHQTCTGPGP PWGLPTCAHS LRPLAGRSGH PGPSPVPWDR120 RCRCHACGTG RGRHRIGPHR PFPSQGQARC SHSLTGTGRA HSGRPSSRRT HKSHTFLHLS180 RTRLLASCLS PNAAPYLSAG 200

(2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

STSHDCVPQA DAAAYSRTAD GETEARGGRG GADLPASPSP RPRLAPPWPV RSTRGARRRR 60
TARGQAGSSS AMAAQRLGKR VLSKLQSPSR ARGPGGSPGG LQKRHARVTV KYDRRELQRR120
LDVEKWIDGR LEELYRGMEA DMPDEINIDE LLELESEEER SRKIQGLLKS CGKPVEDFIQ180
ELLAKLQGLH RQPGLRQPSP SHDGSLSPLQ DRARTAHP

(2) INFORMATION ON SEQ ID NO. 376:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

NQLKLKQQAG SFSQEGCKGE NILSFLLQGN HCPGVPASGR HNLSKVQGML ARKGGILDCC 60 LLSEPSPTPQ PASWCLFSSK LSLPNLSSSE GKRESVPGFS RVGERTGKGT DI 112

(2) INFORMATION ON SEQ ID NO. 377:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

VRPEHSLMVL SLDTPTSYLQ FSRRRASGTL GCKPNLGSMF ALNPNSQRRS ECIFHHAAAG60 CWPRFCVFSQ PSEITSFLVA VTNSSWTTMK LIYFPI 96

(2) INFORMATION ON SEQ ID NO. 378:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

SNRLVASPKK DARVKTFFPS FCREIIALVC QPVVGTTFQK FKGCWLEKEV FWIAASSQNP 60 LLPHSLPPGV FFPPNSLYLT SLHQKASGNL FRVSVEWEKG QAKAQIFRRE SSYFWPLHVP120 YSGIVGPDDW HSDSQLWFWE NIRGS

(2) INFORMATION ON SEQ ID NO. 379:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 429 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

RQFEITSISV DVWHILEFDY SRLPKQSIGQ FHEGDAYVVK WKFMVSTAVG SRQKGEHSVR 60
AAGKEKCVYF FWQGRHSTVS EKGTSALMTV ELDEERGAQV QVLQGKEPPC FLQCFQGGMV120
VHSGRREEEE ENVQSEWRLY CVRGEVPVEG NLLEVACHCS SLRSRTSMVV LNVNKALIYL180
WHGCKAQAHT KEVGRTAANK IKEQCPLEAG LHSSSKVTIH ECDEGSEPLG FWDALGRRDR240
KAYDCMLQDP GSFNFAPRLF ILSSSSGDFA ATEFVYPARA PSVVSSMPFL QEDLYSAPQP300
ALFLVDNHHE VYLWQGWWPI ENKITGSARI RWASDRKSAM ETVLQYCKGK NLKKPAPKSY360
LIHAGLEPLT FTNMFPSWEH REDIAEITEM DTEVSNQITL VEDVLAKLCK TIYPLADLLA420
RPLPEGSIL

(2) INFORMATION ON SEQ ID NO. 380:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

DVFHEGDLIG NFRVHLCDLS DVLSVLPAGK HIGECQGLQT SVDKVRLGGW FLEIFSFAVL 60 EHSLHRTLPV GGPADAGGTS DLVLDGPPAL PEVHLVVIVN KEKCWLGRAV QIFLQEGHGT120 DHRGGSGRVH KLCGCKIPRG AAEDEQAGRE VKTSRILKHA IVGFPVSPS 169

- (2) INFORMATION ON SEQ ID NO. 381:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GIPESEWLGA FITLVYCDFA ATMQSCFQGT LFLDLVRSGP SDLLRVGLGF ASVPQVDEGL 60 VDVKHHHGSS GPQAATVTGH FQQIPFHGHL STHAVQPPLT LHIFFFLFPP PRVHHHPPLE120 TLQETGGLLS LENLDLGPPF LVQLHRHQRR RALLTHGGVP ALPEEVDALL FAGCPHRVLS180 LLATSHCRAH HELPLDHIGI PLMELPDALF GEPAIVEFQD VPDIHGNAGD LKLP 234

- (2) INFORMATION ON SEQ ID NO. 382:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

RLFAPLRTSW AVVIPGARVA LCFYKIMTYV TCLHVCLLVE FLNSQLTNHR KYYFLSYGFW60 FTGLRGFSEY LWPQQHTQFP S 81

- (2) INFORMATION ON SEQ ID NO. 383:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

IVNRTTACTL FEVNLEWKAR DYTLFKIDIC GAHTIYEIVP SKKEKKKIRR SNLEQHCLIK60 A

- (2) INFORMATION ON SEQ ID NO. 384:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

PPDFFFLFFR GYYFIYCVSP TNVYFKKSIV PGLPFQIHLK ESTCSSPVYN LIEMRK 56

- (2) INFORMATION ON SEQ ID NO. 385:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

LDSSHCCSCS TALFRTQTTA AAVPRMVIRV YIASSSGSTA IKKKQQDVLG FLEANKIGFE 60 EKDIAANEEN RKWMRENVPE NSRPATGYPL PPQIFNESQY RGDYDAFFEA RENNAVYAFL120 GLTAPPGSKE AEVQAKQQA 139

- (2) INFORMATION ON SEQ ID NO. 386:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

ETKHILLFLL NRCRARGRCN IYTDHHPGNS GCGCLGPEKG CGAAAAMAGI QLGAETAVGR60 EGWGKVEGEL ARAPPPPLAA STELSKRCSS SPKPR 95

- (2) INFORMATION ON SEQ ID NO. 387:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387;

FCIHFECLHV KTQLIYYFNI KPISFEAKLI LLFYKSNGDS FFRMLKAQCL RFMLAALLAL60 LLPLNQVGLS SLRRHTLHYF LWLQRRHHSP RDTGFH 96 (2) INFORMATION ON SEQ ID NO. 388:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 221 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

FIMLNIILIK FSSFSIRCAI LSSVCLNEAI TFAFLLQVFL WNMDKYTMIR KLEGHHHDVV 60 ACDFSPDGAL LATASYDTRV YIWDPHNGDI LMEFGHLFPP PTPIFAGGAN DRWVRSVSFS120 HDGLHVASLA DDKMVRFWRI DEDYPVQVAP LSNGLCCAFS TDGSVLAAGT HDGSVYFWAT18 FRQVPSLQHL CRMSIRRVMP TQEVQELPIP SKLLEFLSYR I 221

- (2) INFORMATION ON SEQ ID NO. 389:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

KGGATCPESP QDRKRRGNLD MEKLYSENEG MASNQGKMEN EEQPQDERKP EVTCTLEDKK 60 LENEGKTENK GKTGDEEMLK DKGKPESEGE AKEGKSEREG ESEMEEVERE GTRGRGSG 118

- (2) INFORMATION ON SEQ ID NO. 390:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

RFPYLGFPLS RPPPSLTLPP SLTFLLLPLP HSLAFLYPLT FPHLLFCPCF LSFPRFLTSC 60 LPEYKLLLAF SRLVAVLHFP SFLGLKPFLH FHCRVFPCRD FPSFSCPAGI LDRLLLLFSF120 AERWEQQTRR PGRSWTKN 138

- (2) INFORMATION ON SEQ ID NO. 391:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3218 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

CCCTCCTCCT	GCTGGTGCAT	CCATCACTAC	COMMERCECCA	رسسسررررسس _۲ ۷	AACAACCACA	60
						120
	GAGATAAAGA			GATGAAGTGG		
	TATACAAGAC			ACAACCCTTC		180
GTTACAGCCT	GACTTCCAGC	CAGTCTGTGC	TTCACAGCTC		ACAAACATCT	240
TCTGATCAAA	CGGTCCCTGC	GCTGCCGTAA	ATGTGAACAT	AATTTGAGCA	AGCCAGAATT	300
TAACCCAACG	TCAATCAAAT	TCAAAATCCA	GCTGGTCGCT	GTCAATTATA	TTCCAGAAGT	360
GAGAATCATG	TCAATTCCCA	ACCTTCGCTA	CATGAAGGAG	AGCCAGGTCC	TCCTGACTCT	420
TACAAATCCA	GTTGAGAACC	TCACCCATGT	GACTCTCTTC	GAGTGTGAGG	AGGGGGACCC	480
TGATGATATC	AACAGCACTG	CTAAGGTGGT	GGTGCCTCCC	AAAGAGCTCG	TTTTAGCTGG	540
		ACGATGAGTT		CAAGACTTTC	AGGACGATCC	600
	GCCTTCAGAA			TTCATCAAAG	TTACACCACA	660
	GGTGAAGTGA			CATGATTTTA		720
AGCCCCCATT	CGCCCCATTG	AAGAAAGTGA			GGCTCACCCA	780
GCATGTGGAA	CTTAGCTTGG	GCCCACTTCT	TCCTTAAAAG	GTTCCACTGG		840
CCAAAGGACA	GTATCACCGT	AAACCTGCGT	TAAAATGTGG	AAGCTGCTGC		900
CTTGTTTATA	ACGATGTACC	CATGCACTAC	GGAATTCTAT	TGCTAAGAAA	GTGGGAGCAT	960
AGGCAAGGCA	TTGGGAACAC	AGGGTAGCTG	CTGTTGCTCT	TGCTCTCACC	CCTGTTGACA	1020
	TGTGTCTCCC				GCATAATTCC	
		TGTTCCTTGG			CTGAGAAACT	
CTGTACTGTC		ATCTCACTAA			AAACTTAAATI	
	AGGTAGACCT	GCTGTTAATG	ATCCAGCATT	GGTCACAATG	TACCAACTGC	
	CCGTTAAATA					
				TATCCCTTCA		
GGCTGCCATT		TTTCCATATA			CTTTATCTTT	
AGTATCATGA		AACCTGTGAA		CACTCTCATT	TGCCCTCTTT	
TTCTAAGTGA	ATACAGGACA	CGTATTAGTT	GTTCTTAANN	NNNNNNNNN	UNUNUNUNUN	1500
NUNUNUNUN	иииииииии	ииииииииии	NNNNNNNNNN	NNNNCAAGGG	GGTAGCAGAT 1	L560
TCCATTCGTT	TTCAATATTG	CCACAATACC	CAGGGATTAA	TGCTGCCACA	GGGGGGCAATI	L620
CTTTATTTGT	CTTACTTCCT	ACCCCTTCCC	TGTTCTGCCT	CTTTAACTCA	GTTAAGTTGT1	1680
TCTGTTTGGG	ACCTGGAAAA	GAACCCAAAG	AAAACCTGAG	TGGACAGGTT	CATTTCTGGAI	740
ATGCAGAAAA	CATTTTAAAG	GCTAGATTTT	TAGAATATTC	TCAACTAGCA	TTCTTTCCAT1	008
TGATTTGAAG	GGGAAATTAA	CTATTATAAT	CTCTTGAATC	CAAAACTGGA	TATTAAGAAC1	860
	ACTAAGTTTA				ACCATTTTGA1	
	TAAAATAGTT		CCCACAGTTC		GCAGACTTGC1	
TGTTTTCACT		GAGTTGGGTT			TGTTTTCTAA2	
					GTATTGTTAG2	
	GATAAAGTAG		GCACCGTGTT			
	AGAGACTTGA		GATTTTTTGT		CTTGTTTTAA2	
	ATTAAAGATA				AGTCCTTGTA2	
AGCTTCCCTT	GAAAATGTTT	TAAATATTTA	GGAAGCTTTT		AAATTGTACT2	2280
CTAAAAGACA	CTAAATTGTA	CTAATTGTAC	AAAGGTCAAG	CCAATTTTAT	GAAACAGTCC2	2340
TACAGAGTAA	TATATGTGAT	GCAGTGTAAG	AAGGAAAATA	CTCATCTCTA	ACATTATGGT2	2400
AATAACATTT	AGCCTCTTAG	GAGTTGGAGC	AGGGGGATGG	GTAATTACAG	ATTTGCAGAC2	460
TATAGAAAGA	GTTTCATTTT	TTTGTGACCC	CACAGAGTCT	CAAATTTTTA	TTTCACTACC2	2520
TGCTAGAGCC	TACTGTGAAA	TCACTGCTCC	ATATTTGCCA	GTGGAGGAAA	TGGGCATAGA2	2580
					TCATGCGTTT2	
					TCTCATCATT2	
					AGCCAAACTA2	
					TAGTGTAAGC	
					TAGGAATTGT2	
					CAGTATGCAC2	
					ACTTAGGCTA3	
					TGAAGTGCTT3	
					TTGGTCCCTT	
				GTTACTGTTT	TGCCTTATTG	
CTTAACTTAA	TGTAGTGAAA	TAAAGCAGAC	AAAGCTTG		3	3218

(2) INFORMATION ON SEQ ID NO. 392:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

GTGAGGGACA GATGGACAGA ATGCAGAGGT ACATAGATGA GCTGAGGCTG ATCCAGCTCC 60
CCTGAAATTC AGAGTGTTAA CTTTGTAGAC CCTGCACAAT CTCTTGGTGC TATCTAGCCA120
TTACCCCCAT TTTTTTTTA AAGGCCATCT GAAATTCCAT TTGTCATGGT GGGAAGCATT180
TTGGATATGA TGCAGGAAAT CTCTTCCTGG AGTCAAAAGT TCCCAAGAGG TCCTGTATTT240
TTAAGAAATG GAATTTATTT AAATAATATT TAAGCTTTGT CCCATGTTGG CCGGGCAACT300
TTTTTCAATG GTGCTTATTA GAAGAAGTTT TTTCATCTTG TCATTTTAAG AAAATAAAAC360
TGGAAATTGA ATATGGGTGG CATGATTGA CCCTTTTAGT TCTCTTATTT TTCTACTCCT420
CTGTCCCTCT ATAACTATGC CATACTATTA GATGCTGGTC CACTGAATGC TGAGATGATC480
TGTTTTTTGG GGTTTTTTT TTTTAAGAAA TATTTTCACT GGTTTTCTGT GACTCTCTAA540
ACACTTCATC GAAACTAGGA AGACTGAATT ATGAGGGGAA CTATTTGGGA TTAGTGGCCA600
GAAACGATGA AATCTTATAG ATCTTTTGAC AGTTTCTCTG TTTAGGGGGA GCCTAGGACT660
GATATCCAAG TTTCTTCCAT ATCCAAGCTT CATTGGGGA CCCCCATTTG GCTTTAACAG720
GTGACCCGGC CCTCTTTACC GGGCTTCCAG

- (2) INFORMATION ON SEQ ID NO. 393:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CACGAGGAGG CCGGGAGTG AACCCCCTCT TTTGAGAAGG TTGCCTGACT CAGAGACACA 60
GAAACGGGTC CAGGGATGGG GAGAGATGTG GAGTGAGGGA AGGTTTGCAT TTGAGAAAGG120
AAGTTCGAGA ACACACTGGG ACATTGTAAC ACATTTGAAC CATCTTCTGA TAGAAAAGGTG180
TTGGCCTCCT AATAATGGGA GGTCAGGGCC AGGTCCTCGG GCATAGGGAG AGGGTCCGGA240
GAATGCTGCA GACCCCTGCC CACTGCCCAC GGTCTCCGCT CCCTGCACCT GCCTCTGATG300
GTGCAGCTCT GATTCCGTGT CTCTCCTCAT TGCAGATTA TGAAGGTGCC TACCATGTTC360
TCCACAAAGGA GCTTCCTGAA GTCACCAACT CCGTCTTCCA TGAAATAAAC ATGTGGGTCT420
CTCAAAAGGAC AGCCACGGCA GGAACTGCGT CCCCACCCTG AATGCATTGG CCGGTGCCCG480
GCTCATGGTC TGGGGGATGC AGGCAGGGGA AGGCCAGAGA TGGCTTTCTCA GATATGGCTT540

GCAAAA 546

- (2) INFORMATION ON SEQ ID NO. 394:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2453 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

CCTGACGGGA	CCAAGGCGGC	GGGAGTCTGC	GGTCGTTCCC	TCGGCTGTGG		60
ACGACGCGGT	GCAGGGTAAC	ATGGCGGATG	CGGAAGTAAT	TATTTTGCCA	AAGAAACATA	120
AGAAGAAAAA	GGAGCGGAAG	TCATTGCCAG	AAGAAGATGT	AGCCGAAATA	CAACACGCTG	180
AAGAATTTTT	TATCAAACCT	GAATCCAAAG	TTGCTAAGTT	GGACACGTCT	CAGTGGCCCC	240
TTTTGCTAAA	GAATTTTGAT	AAGCTGAATG	TAAGGACAAC	ACACTATACA	CCTCTTGCAT	300
GTGGTTCAAA	TCCTCTGAAG	AGAGAGATTG	GGGACTATAT	CAGGACAGGT	TTCATTAATC	360
TTGACAAGCC	CTCTAACCCC	TCTTCCCATG	AGGTGGTAGC	CTGGATTCGA	CGGATACTTC	420
GGGTGGAGAA	GACAGGGCAC	AGTGGTACTC	TGGATCCCAA	GGTGACTGGT	TGTTTAATCG	480
TGTGCATAGA	ACGAGCCACT	CGCTTGGTGA	AGTCACAACA	GAGTGCAGGC	AAAGAGTATG	540
TGGGGATTGT	CCGGCTGCAC	AATGCTATTG	AAGGGGGGAC	CCAGCTTTCT	AGGGCCCTAG	600
AAACTCTGAC	AGGTGCCTTA	TTCCAGCGAC	CCCCACTTAT	TGCTGCAGTA	AAGAGGCAGC	660
TCCGAGTGAG	GACCATCTAC	GAGAGCAAAA	TGATTGAATA	CGATCCTGAA	AGAAGATTAG	720
GAATCTTTTG	GGTGAGTTGT	GAGGCTGGCA	CCTACATTCG	GACATTATGT	GTGCACAGTG	780
ATCAGTCACG	CGCACGAGGT	ACGTCAGATG	CAGGAGCTTC	GGAGGGTTCG	TTCTGGAGTC	840
ATGAGTGAAA	AGGACCACAT	GGTGACAATG	CATGATGTGC	TTGATGCTCA	GTGGCTGTAT	900
	AGGATGAGAG	TTACCTGCGG	CGAGTTGTTT	ACCCTTTGGA	AAAGCTGTTG	960
ACATCTCATA	AACGGCTGGT	TATGAAAGAC	AGTGCAGTAA	ATGCCATCTG	CTATGGGGCCI	1020.
AAGATTATGC	TTCCAGGTGT	TCTTCGATAT	GAGGACGGCA	TTGAGGTCAA	TCAGGAGATT1	
	CCACCAAAGG	AGAAGCAATC	TGCATGGCTA	TTGCATTAAT	GACCACAGCG1	
GTCATCTCTA	CCTGCGACCA	TGGTATAGTA	GCCAAGATCA	AGAGAGTGAT	CATGGAGAGAI	1200
GACACTTACC	CTCGGAAGTG	GGGTTTAGGT	CCAAAGGCAA	GTCAGAAGAA	GCTGATGATC1	
AAGCAGGGCC	TTCTGGACAA	GCATGGGAAG	CCCACAGACA	GCACACCTGC	CACCTGGAAG1	
CAGGAGTATG	TTGACTACAG	TGAGTCTGCC	AAAAAAGAGG	TGGTTGCTGA	AGTGGTAAAA1	
GCCCCGCAGG	TAGTTGCCGA	AGCAGCAAAA	ACTGCGAAGG	GAAGCGAGGA	GAGTGAGAGT1	
GAAAGTGACG	AGACTCCTCC	AGCAGCTCCT	CAGTTGATCA	AGAAGGAAAA	GAAGAAGAGT I	
AAGAAGGACA	AGAAGGCCAA	AGCTGGTCTG	GAGAGCGGGG		AGATGGGGAC1	
	CCAAGAAGAA			AAGAGGTAGA		
GAGTAGTGAA	GGCCACTTGA	AGCTGGAGGA	GAAACTAAAG	CCTTATTGAG	AAAACATGTT1	
ATAGATCCTT	TTGTTGCTGA	GAGAGTGGAA	CATAGGTCCT	AGACAGGGTG	AAGAGTTCTG1	
GCACATTTTA	GCTGCTACTT	TGAGACCTCG	GTGATGTTAC	CTGGTGTGGT	CATCCCATCTI	
TGTCCTGTTT	TAAGGATATG		GATGAAAGAG	GCAGAGTTTA	TCCCAATGAC	
TTCTCTGTTT	GAGTTGGGAA	GCCTCACCTT	CAGACCCAGT	AACTGTCCGC	AGCTGTCTGC	1920
TAGTGGTTGT	CTTAACATCG	TAGTCCTAGT	TTGCATTTTT	TAAATCCCCT	CTGTTTAAAA	1980
GGTTTGTAAA	ACAAAAACAA	AAAACTAAGT	CTGCTCAGTG	AAATGCTGTA	GAACCCTAAA.	2040
TAAGTGGTAG	AAGAGTGTCA	CTGAATTTTG	TCTCTGAATT	CAGTATAACT	GAGTTTTGTC	2100
CATGCTGGTG	TCTGGGTTAT	AGGCCTGATG	GGCCTGGTAG	TTTTCCATCT	TGTTCTGGCC	2160
TAGAGGTCAG	TCCTTTGCAC	TTCCTCAAAG	CTTGTGTACA	GTGCTCACCT	AAATCCATCT:	2220
GACTACTTGT	TCCTGTGCCC	TCTTGTTTTA	GGCCTCGTTT	ACTTTTAAAA	AATGAAATTG:	2280
TTCATTGCTG	GGAGAAGAAT	GTTGTAATTT	TTACTTATTA	AAGTCAACTT	GTTAAGTTTT	2340
TTATGTATTC	CTGTTGGGTT	TTCTTGTTGA	TCTCATGCTA	GCAGAGCAAA	AATTGTAAAA	2400
TATTTTGATT	AAAAATCTAG	GGACCTTTAT	GTCCTATTTG	AAAAAAAAA	AAA	2453

(2) INFORMATION ON SEQ ID NO. 395:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2706 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GGGAGGAAGG AGACTACACC TGCTTTGCTG AAAATCAGGT CGGGAAGGAC GAGATGAGAG TCAGAGTCAA GGTGGTGACA GCGCCCGCCA CCATCCGGAA CAAGACTTAC TTGGCGGTTC 120 AGGTGCCCTA TGGAGACGTG GTCACTGTAG CCTGTGAGGC CAAAGGAGAA CCCATGCCCA 180 AGGTGACTTG GTTGTCCCCA ACCAACAGG TGATCCCCAC CTCCTCTGAG AAGTATCAGA 240 TATACCAAGA TGGCACTCTC CTTATTCAGA AAGCCCAGCG TTCTGACAGC GGCAACTACA 300 CCTGCTTGGT CAGGAACAGC GCGGGAGAGG ATAGGAAGAC GGTGTGGATT CACGTCAACG 360 TCCAGCCACC CAAGATCAAC GGTAACCCCA ACCCCATCAC CACCGTGCGG GAGATAGCAG 420 CCGGGGGCAG TCGGAAACTG ATTGAGTGCA AAGCTGAAGG CATCCCCACC CCGAGGGTGT 480 TATGGGCTTT TCCCGAGGGT GTGGTTCTGC CAGCTCCATA CTATGGAAAC CGGATCACTG 540 TCCATGGCAA CGGTTCCCTG GACATCAGGA GTTTGAGGAA GAGCGACTCC GTCCAGCTGG 600 TATGCATGGC ACGCAACGAG GGAGGGGAGG CCAGGTTGAT CCTGCAGCTC ACTGTCCTGG 660 AGCCCATGGA GAAACCCATC TTCCACGACC CGATCAGCGA GAAGATCACG GCCATGGCGG 720 GGCCACACA TTCAGCCTCA ACTGCTCTGC CGCGGGGACC CCGACACCCA GCCTGGTGTG 780 GGTCCTTCCC AATGGCACCG ATCTGCAGAG TGGACAGCAG CTGCAGCGCT TCTACCACAA 840 GGCTGACGGC ATGCTACACA TTAGCGGTCT CTCCTCGGTG GACGCTGGGG CCTACCGCTG 900 CGTGGCCCGC AATGCCGCTG GCCACACGGA GAGGCTGGTC TCCCTGAAGG TGGGACTGAA 960 GCCAGAAGCA AACAAGCAGT ATCATAACCT GGTCAGCATC ATCAATGGTG AGACCCTGAA1020 GCTCCCCTGC ACCCCTCCG GGGCTGGGCA GGGACGTTTC TCCTGGACGC TCCCCAATGG1080 CATGCATCTG GAGGGCCCCC AAACCCTGGG ACGCGTTTCT CTTCTGGACA ATGGCACCCT1140 CACGGTTCGT GAGGCCTCGG TGTTTGACAG GGGTACCTAT GTATGCAGGA TGGAGACGGA1200 GTACGGCCCT TCGGTCACCA GCATCCCCGT GATTGTGATC GCCTATCCTC CCCGGATCAC1260 CAGCGAGCCC ACCCCGGTCA TCTACACCCG GCCCGGGAAC ACCGTGAAAC TGAACTGCAT1320 GGCTATGGGG ATTCCCAAAG CTGACATCAC GTGGGAGTTA CCGGATAAGT CGCATCTGAA1380 GGCAGGGGTT CAGGCTCGTC TGTATGGAAA CAGATTTCTT CACCCCCAGG GATCACTGAC1440

CATCCAGCAT GCCACACAGA GAGATGCCGG CTTCTACAAG TGCATGGCAA AAAACATTCT1500 CGGCAGTGAC TCCAAAACAA CTTACATCCA CGTCTTCTGA AATGTGGATT CCAGAATGAT1560 TGCTTAGGAA CTGACAACAA AGCGGGGTTT TTAAGGGAAG CCAGGTTGGG GAATAGGAGC1620 TCTTAAATAA TGTGTCACAG TGCATGGTGG CCTCTGGTGG GTTTCAAGTT GAGGTTGATC1680 TTGATCTACA ATTGTTGGGA AAAGGAAGCA ATGCAGACAC GAGAAGGAGG GCTCAGCCTT1740 GCTGAGACAC TTTCTTTTGT GTTTACATCA TGCCAGGGGC TTCATTCAGG GTGTCTGTGC1800 TCTGACTGCA ATTTTTCTTT TTTTGCAAAT GCCACTCGAC TGCCTTCATA AGCGTCCATA1860 GGATATCTGA GGAACATTCA TCAAAAATAA GCCATAGACA TGAACAACAC CTCACTACCC1920 CATTGAAGAC GCATCACCTA GTTAACCTGC TGCAGTTTTT ACATGATAGA CTTTGTTCCA1980 GATTGACAAG TCATCTTTCA GTTATTCCTC TGTCACTTCA AAACTCCAGC TTGCCAATAA2040 GGATTTAGAA CCAGAGTGAC TGATATATAT ATATATTTTA ATTCAGAGTT ACATACATAC2100 AGCTACCATT TTATATGAAA AAAGAAAAAC ATTTCTTCCT GGAACTCACT TTTTATATAA2160 TGTTTTATAT ATATTTTTT TCCTTTCAAA TCAGACGATG AGACTAGAAG GAGAAATACT2220 TTCTGTCTTA TTAAAATTAA TAAATTATTG GTCTTTACAA GACTTGGATA CATTACAGCA2280 GACATGGAAA TATAATTTTA AAAAATTTCT CTCCAACCTC CTTCAAATTC AGTCACCACT2340 GTTATATTAC CTTCTCCAGG AACCCTCCAG TGGGGAAGGC TGCGATATTA GATTTCCTTG2400 CTGCATCATA ACTTTACAGA ATTGAATCTA GAGTCTTCCC CGAAAAGCCC AGAAACTTCT2520 CTGCAGTATC TGGCTTGTCC ATCTGGTCTA AGGTGGCTGC TTCTTCCCCA GCCATGAGTC2580 AGTTTGTGCC CATGAATAAT ACACGACCTG TTATTTCCAT GACTGCTTTA CTGTATTTTT2640 2706 AAAAAG

(2) INFORMATION ON SEQ ID NO. 396:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2242 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

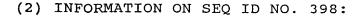
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

					·	
CAGGCCGGTT	CCGGCGAAGT	TAAACCCTCG	GAGCTGGCCT	CGGACTGCTG	GGGCGTTACC	60
CCTTCGGCCA	CCCCCCCTGA	CCATGGCAGT	GTTTCATGAC	GAGGTGGAAA	TCGAGGACTT	120
CCAATATGAC	GAGGACTCGG	AGACGTATTT	CTATCCCTGC	CCATGTGGAG	ATAACTTCTC	180
CATCACCAAG	GAAGATTTGG	AGAATGGGGA	AGACGTGGCA	ACGTGTCCTA	GCTGCTCTCT	240
CATTATAAAA	GTGATTTATG	ACAAAGATCA	GTTTGTGTGT	GGAGAAACAG	TCCCAGCCCC	300
TTCAGCCAAC	AAAGAATTAG	TTAAATGCTG	AAGAAGCCTT	CAGGAATCCA	AATCCTGAAC	360
ATTTGGAATG	AGCCCAGATA	. GAAATATCGA	ATGCAAAGCT	ACTGGCTTCA	CAGAGACAAC	420
CATTTATGAT	TTGCTGTTCT	GTAAGAGTGT	GGATTCTTTC	TATCAACTGC	TGATATCATC	480
TTCAGGAAGC	AAGTCCATAA	. CATGACATAT	CTGGATTTTG	TGCTTAGAAC	CTTAAATTGG	540
AAGCATTCTT	AATTATGCAT	CTAAATTTAA	AAGAAGATAA	TTTCAAAACA	GTGCTTTCTT	600
TCCCTTGGTT	TCATCATTTT	CATATCTTAA	ACCAAATTAC	TTCGGTATCT	GACAACAGCA	660
TCATCTACCT	CAGTCATTAG	GATTTCTTAA	TAAAAAAGAG	ATTGTATTTT	TGACTTGGTT	720
ATTAAGATTA	TTAAAATTAG	CCCTTCCTTT	GAAATATGAC	ATCAGCTTTG	CTGTTCTAAA	780
TTTAAAATTA	GTTGCTTCAT	CAGTACCACA	CTTCCAGTTT	CTATACCAAG	CCAGTCTCCT	840
CAGTTTTCCC	ATTAGAATGG	ACATGTTCTG	TTCAGCGTGT	CATTTCTGTA	ATGCTTCATG	900
CAGAGAGTTT	GGTCATAGTA	TTAAAGAGAA	AATACAGTGA	GGTCACAATG	TCTCCAGAGC	960
TAAAAGTTAG	TGAACAAGAA		AAATGAAGTG	ATGAAAGAAT	GAGGACTTTT1	.020
CTTATATTCT	GCATATTCCT	TGGAAGTCAG	GACAAGATGA	AAAGAAAAAC	ATCCAAAAGA1	.080
AGTGAAATTG	GTGACAGAAT	GAGAGGAGCA	AAGCATACCA	GTGTAGTAAG	TGGAATGTTT1	.140
GAATGACTTT	GCCAGGTCAG	AGCAAGTAAT	ATTTCTGTAT	CTGAGTTTTT	GTTTGTGTTT1	.200
TGATAAGGCT	AATGAAATTG	CATTCCAGGT	AGGGGTTAAC	GTCAAATTTC	CATGGCTGGT1	.260
AGCTGTGCTT	TTGGCATATC	ACAGTGTTGT	GTCACTACTA	CAAGGTAAAG	CATCTACAGC1	.320
GGAGAATGAG	CTTGAAAATG	AGAGACCTAT	TGTGAATAAA	TATGCCCATG	AGAGCATATT1	.380
TAATAAGCCT	CTATAACATG	CAGCCAAACC	AGACATTCAC	TCCTGCAGAG	AAATGTTGCC1	440
CTGGAGAAAA	AGAGATATAT	AAAGATAGGC	TATCACCCTT	CTTTTGCTGC	AGTACTAAGC1	500
ATAGCAAGAA	ATTAGAATCA	TTTACATTGG	AAATTTGAAA	ATTCCCTTTA	TATACACAAC1	560
TTTACTGTGT	ATAAATAAAA	AATATTTATT	AATGCAGTGA	TGTCCGTCAG	GTTGTTTTAG1	620
GAATGGCTTC	TGCAATTAGA	AAAATAGCTT	GCTAGAATGT	AAATGTTCTG	CTACTGGTAA1	680
ATGTACTGCA	CACATTCATT	GGACGTTAAA	ACAAGTGAGT	AGCCTTTTTT	ACCTGCCAGC1	740
AGCATGGCTG	TGTGCAGCCA	CTAGGCTGAG	ACAATAAATT	ACCAAAAATT	ATAATGTACC1	800
GAGCTGAAAA	TGCTCAGTAC	ATTATGTGGC	ATATTCTGGA	TGTGATGAGA	AATCTCATTG1	860
CCATTTGGGA	CACTGACATC	CCAGAAGTAA	TCCACAACTG	CTTTGCAAAA	GCAAAGTGAC1	920
TGCTCAGATG	AACAGAGCAG	AGTACTCACT	CACTATGGTG	GCATCAGCTG	CAAAGCGAAA1	980
TGAACTGTCC	CATGATCATG	TTGATGGTTT	TCTAGATACT	GCCAACATGT	TAGCTCTTTC2	040
TGATGCTGAT	GAGTTTCAAA	CACGAACAGA	CANCCTTGAT	GTGGGTTTGC	TAAGAACATA2	100
GAAGAACAGG	AAGAAAAGTT	GCCAGGGTTT	AAAAATCCCA	GGGAAAAAAG	AAGCATAAAA2	160
AGCATTAGCA	GTCAGTGACT	GATGATAATG	CTTGCAATAA	TGGGGAATGG	TTTTGTTTTC2	220
TAAAACCCAA	AATTTATTTC	TT	•		2	242



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1239 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

TAGTCATCCT ACAAACATGT TTCTGTTACT TCCTAATATT AAAATAGCCA TTTTGGATTC CATATTTAAA GTGCTCATTT GAGTGAAATT CAAATTAGAA AGAAAGATAT TAAAATGCGC 120 CTAACAAAAA CCTCTCTTTC AGAATCCCTA TTCCTTGAAT CTTGGGTTTG AACTGCTTAT 180 TAAAGGCAGG CCTAAACTAA TTTGTGAGAA ATGAAGAAGT TTTAGTATAT AATTCTTTTA 240 AAAAATATCA ATTACGGCTG GGTGCGGTGG CTCAGGCCTG TAATGCCAGC ACTTTGGGAG 300 GCCAAGGCGG GTGATCACCT GAGGTCAGGA GTTCAAGACC AGCCTGGCCA ACATGGCAAA 360 ACCCTGTCTC TACTAAAAAG TAAAAAAAT TAGCCGGGCA TGGTGGCTTG TGCTTGTAGT 420 CCCACTTCAG TCTAAGTAGC TGGGACTACA GGCACGTGCC ACNAGGCCCA GCTAATGTGG 480 GTGTTTTGTT AGAGATGAGG TAGGGCCATA TTGCCCAGGC TCGTCTTGAA CACCGGGGCT 540 CAAGGAATCT GCCCATCTTC GCCTCCCAAA GTTCTGAGAT AGCAGGTGTG AGTCANTCAT 600 GCCCAGCCTC CTTGAAGTTT ACTAACAATT GGGATAACTG AGGGAAGAGA AGTGACAATT 660 CCACTCAGTC TATTAGAGGT CTGGATATAA GGTAGNCCAC ACAATAACTC TAACNTTGAC 720 TTCTAACCAT TCTATCTTAT TGNATTTGGA GGCTGTCTTC TGNCCAGATT TTTTGTGGCT 780 TGAGATGATA TTTTNCGAAC CCTTCTTTCA CTACCTTTCT TACCCTTAAT GTGNCCAAGC 840 TTGAAACAGG ATTTGATTTC CTGAGCNTAC TTGTTCNGCC TTCTGTGCGT CANCCAAGTA 900 ATCTGGTTCA TCTTTNCGTN CTCATTCATG TTATTTTCAA GTGAAACAAG ACATTTTGGG 960 GGNTCAAGTC TCNTTTGGGN NTGTTTTGTT TTTATGTATA TAAAAATGGA TTTTGNTGTT1020 CCCTTTCCNA TGTNAAGTAN CCAACTTATA TGGAAACTCA CAATCATAAT GTAAAGAAGA1080 AATGAAANGC CTGGTGTATT GTACTTCAAG ATGCCTCCCT GNATGTATAG AATCNTCCTT1140 GTAAAATAAA TAATTGNCAT TGTATATCAG TCTTCCCATC AATATTAATT ATTAAATATT1200



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1663 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GAACCTGCTC TCCTGCTTGC TGGTCCCTTG ACGCAGAGAC CGTTGCCTCC CCCACAGCCG TTTGACTGAA GGCTGCTCTG GAGACCTAGA GTAAAACGGC TGATGGAAGT TGTGGGACCC 120 ACTTCCATTT CCTTCAGTCA TTAGAGGTGG AAGGGAGGGG TCTCCAAGTT TGGAGATTGA 180 GCAGATGAGG CTTGGGATGC CCCCTGCTTT GACTTCAGCC ATGGATGAGG AGTGGGATGG 240 CAGCAAGGTG GCTCCTGTGG CAGTGGAGTT GTTGCCAGAA ACAGTGGCCA GTTGTATCGC 300 CTATAAGACA GGGTAAGGTC TGAAGAGCTG AGCCTGTAAT TCTGCTGTAA TAATGATAGT 360 GCTCAAGAAG TGCCTTGAGT TGGTGTACAG TGCCATGGCC AGCAAGAATC CCAGATTTCA 420 GGTTTTATTA CAAAATGTAA GTGGTCACTT GGCGATTTTG TAGTACATGC ATGAGTTACC 480 TTTTTTCTCT ATGTCTGAGA ACTGTCAGAT TAAAACAAGA TGGCAAAGAG ATCGTTAGAG 540 TGCACAACAA AATCACTATC CCATTAGACA CATCATCAAA AGCTTATTTT TATTCTTGCA 600 CTGGAAGAAT CGTAAGTCAA CTGTTTCTTG ACCATGGCAG TGTTCTGGCT CCAAATGGTA 660 GTGATTCCAA ATAATGGTTC TGTTAACACT TTGGCAGAAA ATGCCAGCTC AGATATTTTG 720 AGATACTAAG GATTATCTTT GGACATGTAC TGCAGCTTCT TGTCTCTGTT TTGGATTACT 780 GGAATACCCA TGGGCCCTCT CAAGAGTGCT GGACTTCTAG GACATTAAGA TGATTGTCAG 840 TACATTAAAC TTTTCAATCC CATTATGCAA TCTTGTTTGT AAATGTAAAC TTCTAAAAAT 900 ATGGTTAATA ACATTCAACC TGTTTATTAC AACTTAAAAG GAACTTCAGT GAATTTGTTT 960 TTATTTTTTA ACAAGATTTG TGAACTGAAT ATCATGAACC ATGTTTTGAT ACCCCTTTTT1020 CACGTTGTGC CAACGGAATA GGGTGTTTGA TATTTCTTCA TATGTTAAGG AGATGCTTCA1080 AAATGTCAAT TGCTTTAAAC TTAAATTACC TCTCAAGAGA CCAAGGTACA TTTACCTCAT1140 TGTGTATATA ATGTTTAATA TTTGTCAGAG CATTCTCCAG GTTTGCAGTT TTATTTCTAT1200 AAAGTATGGG TATTATGTTG CTCAGTTACT CAAATGGTAC TGTATTGTTT ATATTTGTAC1260 CCCAAATAAC ATCGTCTGTA CTTTCTGTTT TCTGTATTGT ATTTGTGCAG GATTCTTTAG1320 GCTTTATCAG TGTAATCTCT GCCTTTTAAG ATATGTACAG AAAATGTCCA TATAAATTTC1380 CATTGAAGTC GAATGATACT GAGAAGCCTG TAAAGAGGAG AAAAAAACAT AAGCTGTGTT1440 TCCCCATAAG TTTTTTTAAA TTGTATATTG TATTTGTAGT AATATTCCAA AAGAATGTAA1500 ATAGGAAATA GAAGAGTGAT GCTTATGTTA AGTCCTAACA CTACAGTAGA AGAATGGAAG1560 АТАССТТССА АТСАААААА ААААААААА АААААААА ААА



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2889 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GATCAGGCCT GTGGTCCAGC TCACTGCCAT TGAGATTCTA GCTTGGGGCT TAAGAAATAT GAAAAACTTC CAGATGGCTT CTATCACATC CCCCAGTCTT GTTGTGGAGT GTGGAGGAGA 120 AAGGGTGGAA TCGGTGGTGA TCAAAAACCT TAAGAAGACA CCCAACTTTC CAAGTTCTGT 180 TCTCTTCATG AAAGTGTTCT TGCCCAAGGA GGAATTGTAC ATGCCCCCAC TGGTGATCAA 240 GGTCATCGAC CACAGGCAGT TTGGGCGGAA GCCTGTCGTC GGCCAGTGCA CCATCGAGCG 300 CCTGGACCGC TTTCGCTGTG ACCCTTATGC AGGGAAAGAG GACATCGTCC CACAGCTCAA 360 AGCCTCCCTG CTGTCTGCCC CACCATGCCG GGACATCGTT ATCGAAATGG AAGACACCAA 420 ACCATTACTG GCTTCTAAGC TGACAGAAAA GGAGGAAGAA ATCGTGGACT GGTGGAGTAA 480 ATTTGATGCT TCCTCAGGGG AACATGAAAA ATGCGGACAG TATATTCAGA AAGGCTATTC 540 CAAGCTCAAG ATATATAATT GTGAACTAGA AAATGTAGCA GAATTTGAGG GCCTGACAGA 600 CTTCTCAGAT ACGTTCAAGT TGTACCGAGG CAAGTCGGAT GAAAATGAAG ATCCTTCTGT 660 GGTTGGAGAG TTTAAGGGCT CCTTTCGGAT CTACCCTCTG CCGGATGACC CCAGCGTGCC 720 AGCCCCTCCC AGACAGTTTC GGGAATTACC TGACAGCGTC CCACAGGAAT GCACGGTTAG 780 GATTTACATT GTTCGAGGCT TAGAGCTCCA GCCCCAGGAC AACAATGGCC TGTGTGACCC 840 TTACATAAAA ATAACACTGG GCAAAAAAGT CATTGAAGAC CGAGATCACT ACATTCCCAA 900 CACTCTCAAC CCAGTCTTTG GCAGGATGTA CGAACTGAGC TGCTACTTAC CTCAAGAAAA 960 AGACCTGAAA ATTTCTGTCT ATGATTATGA CACCTTTACC CGGGATGAAA AAGTAGGAGA1020 AACAATTATT GATCTGGAAA ACCGATTCCT TTCCCGCTTT GGGTCCCACT GCGGCATACC1080 AGAGGAGTAC TGTGTTTCTG GAGTCAATAC CTGGCGAGAT CAACTGAGAC CAACACAGCT1140 GCTTCAAAAT GTCGCCAGAT TCAAAGGCTT CCCACAACCC ATCCTTTCCG AAGATGGGAG1200

TAGAATCAGA TATGGAGGAC GAGACTACAG CTTGGATGAA TTTGAAGCCA ACAAAATCCT1260 GCACCAGCAC CTCGGGGCCC CTGAAGAGCG GCTTGCTCTT CACATCCTCA GGACTCAGGG1320 GCTGGTCCCT GAGCACGTGG AAACAAGGAC TTTGCACAGC ACCTTCCAGC CCAACATTTC1380 CCAGGGAAAA CTTCAGATGT GGGTGGATGT TTTCCCCAAG AGTTTGGGGC CACCAGGCCC1440 TCCTTTCAAC ATCACACCC GGAAAGCCAA GAAATACTAC CTGCGTGTGA TCATCTGGAA1500 CACCAAGGAC GTTATCTTGG ACGAGAAAAG CATCACAGGA GAGGAAATGA GTGACATCTA1560 CGTCAAAGGC TGGATTCCTG GCAATGAAGA AAACAAACAG AAAACAGATG TCCATTACAG1620 ATCTTTGGAT GGTGAAGGGA ATTTTAACTG GCGATTTGTT TTCCCGTTTG ACTACCTTCC1680 AGCCGAACAA CTCTGTATCG TTGCGAAAAA AGAGCATTTC TGGAGTATTG ACCAAACGGA1740 ATTTCGAATC CCACCCAGGC TGATCATTCA GATATGGGAC AATGACAAGT TTTCTCTGGA1800 TGACTACTTG GGTTTCCTAG AACTTGACTT GCGTCACACG ATCATTCCTG CAAAATCACC1860 AGAGAAATGC AGGTTGGACA TGATTCCGGA CCTCAAAGCC ATGAACCCCC TTAAAGCCAA1920 GACAGCCTCC CTCTTTGAGC AGAAGTCCAT GAAAGGATGG TGGCCATGCT ACGCAGAGAA1980 AGATGGCGCC CGCGTAATGG CTGGGAAAGT GGAGATGACA TTGGAAATCC TCAACGAGAA2040 GGAGGCCGAC GAGAGGCCAG CCGGGAAGGG GCGGGACGAA CCCAACATGA ACCCCAAGCT2100 GGACTTACCA AATCGACCAG AAACCTCCTT CCTCTGGTTC ACCAACCCAT GCAAGACCAT2160 GAAGTTCATC GTGTGGCGCC GCTTTAAGTG GGTCATCATC GGCTTGCTGT TCCTGCTTAT2220 CCTGCTGCTC TTCGTGGCCG TGCTCCTCTA CTCTTTGCCG AACTATTTGT CAATGAAGAT2280 TGTAAAGCCA AATGTGTAAC AAAGGCAAAG GCTTCATTTC AAGAGTCATC CAGCAATGAG2340 AGAATCCTGC CTCTGTAGAC CAACATCCAG TGTGATTTTG TGTCTGAGAC CACACCCCAG2400 TAGCAGGTTA CGCCATGTCA CCGAGCCCCA TTGATTCCCA GAGGGTCTTA GTCCTGGAAA2460 GTCAGGCCAA CAAGCAACGT TTGCATCATG TTATCTCTTA AGTATTAAAA GTTTTATTTT2520 CTAAAGTTTA AATCATGTTT TTCAAAATAT TTTTCAAGGT GGCTGGTTCC ATTTAAAAAT2580 CATCTTTTA TATGTGTCTT CGGTTCTAGA CTTCAGCTTT TGGAAATTGC TAAATAGAAT2640 TCAAAAATCT CTGCATCCTG AGGTGATATA CTTCATATTT GTAATCAACT GAAAGAGCTG2700 TGCATTATAA AATCAGTTAG AATAGTTAGA ACAATTCTTA TTTATGCCCA CAACCATTGC2760 TATATTTTGT ATGGATGTCA TAAAAGTCTA TTTAACCTCT GTAATGAAAC TAAATAAAAA2820 TGTTTCACCT TTAAAACATA GGGGGGGTGG TCGGGGGGGTC GGGAGGGGG GGGGTGGTGT2880 GGGGTGTGG

(2) INFORMATION ON SEQ ID NO. 400:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1774 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

TGAAGGAAGT AACAAAAGTG GGAAACCCCT GATAAACCCC CTCAGGATCC TCATGGAGAA CTTACCTATC CAGGAGAAAT AGCAAAGGGG AAAGAACTGG CCCCCCCTG ATTCCGATGA 120 CCCTCCCCC GGGTCCCCTC CCCACAACAT GTGGGAATTC CCAGAAGATA AATTCAAGTT 180 GCAATTTCAG TGGGGACATA GCCCAAACCC ATATCACTGG TGATGCCCAC TTCTTCAGTA 240 TTAGGGATTC TCAGTCAGAA GAGACCCCCT GTGTGGCCTG AGTCCCCTCA GGAGGAAGGT 300 GGACAACAGA GAAATGAGAG TTTTGATATT TTCTGAAAGA GGAACATGTG TTAGAGATGA 360 AGAATCTTCC AAGGCTCATG CAGTTGCTTA GAATAATCAT TACTGTTATA TGAGAAACAT 420 TTTAGTAATT TAATAAAAGG ATAATGTTTA TTTAAAAAAC CTGACTTTTC CAGAGTAATT 480 TTGTTTTGCA CATTCATGTT TATTGAAGTG GACTAATTTC TATAATGCAA ATCAGAGTTA 540 AATATTAAAA ATTGTGTAAA TACAATTGAC ATAGGAATTA CATTAAAATA TTAGGAAGAA 600 ACAAGGACAA ATTTAGACCT TGAATCCGAA GAGATAAAGC TTACTTGACT TTCAAATGGA 660 GAGATGATGA AAACCCACTC ATTCAGTCTT TCAGAACAAA AAGACAGTCA TCTGATAAGA 720 GTATGACATG GATGAAATGC CCTACAGGGG CCTTGGACAT CTTTAATTTC TGCGATTATG 780 TGAAAGAGGT GGACTTTACA GATAATGGAG CAGAAGCCAA CATTAGTAAA AGGAATCCCA 840 ACTTCTTCCC ATAGAATTAG AAACATGTGA AAGTACAATA AACTTCTTGT TCAAATTACC 900 AGCATCAGAG AGCTTCCCAT TTGCATCTAG ACCTTGAATT TATATTTATT GATCAAGTTC 960 TAATTTGTAT GTATATTTTG TGCATATTCA CCAATAACAG TTAAAATTAA TTATGTGTTA1020 TAGTTAATAT ATGCACCTAC CTTCTTCCGT TAGTGCATCA GTAAATGTGT TATTTTGTCA1080 TTTTTCCAAA GAGAGTGTTG TAGGTTTTCC CTGTAGTTCT TCCTTTATAG CTTTTCTT1140 GATAACCATG ACTTCAGGAG CTTTAAAACT ATCTATCTTG CATTTGTGTC TGGCGGAGAA1200 CTAGCCATCA GCCTCCTGAA GCCTGCCATC ATTGTTAATT TGAGGACTGG GCTGTCTTGG1260 GGCTCAGAAG GTAAAGAACT ATTTGAGCAG ATGTGTGTG GTGGCACTGG ATTCCACCCA1320 ACTGCCAAGT TAGTATTGTT AGAGATTTCA TTTTACAACA CAAAAATAAG CCTGTGTCAA1380 AGATTTTAAA ATCATGGAAA GTTAAAATCT AGAAAGACCT TAGAGAACCA GCCAACCAAC1440 TCTCTCATTT TAAAAGTGAA GGATTCATAG CACAGATTAC TTGCCTAAGA TCATCCAGGA1500 ACGAAGACAA GAATCCAAAT GTACTTGGGG ACAAGAATTA GTCCCCAAAT TCAGTGTTCT1560 TCCTAGTATT AAACATTGCC CCTTTCGACA AATTTTGGAT TTCAATCTTG GTATATTTCA1620 GTAAACCTGC TGATTTATTA GGTTACTGGG TAGATGACAT TAGAATGTAG ATAGCGTGCA1680 CGCTATGATA GACTCTGCTA AGACATGTTC CCAGTGTCCA GCAGCAATGT AGATATGTGT1740 GACAGTGGTC ATGTAGAAGT TATAAAGCAG AGTA

(2) INFORMATION ON SEQ ID NO. 401:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3982 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

CCCAAGTGTG	ATGCATTGTT	CTTCAGATGT	TGAAAAGAAA	GCAAAAAATA	CCTTCTAACT	60
TAAGACAGAA	TTTTTAACAA	AATGAGCAGT	AAAAGTCACA	TGAACCACTC	CAAAATCAGT	120
GCATTTTGCA	TATTTTTAAA	CAAAGACAGC	TTGTTGAATA	CTGAGAAGAG	GAGTGCAAGG	180
AGAAGGTCTG	TACTAACAAA	GCCAAATTCC	TCAAGCTCTT	ACTGGACTCA	GTTCAGAGTG	240
GTGGGCCATT	AACCCCAACA	TGGAATTTTT	CCATATAAAT	CTCAATGAAT	TCCCTTTCAT	300
	AAACCCAAAT	CCATGCAAGT	GTTTTAAAGC	ACTGTCCTGT	CTTAATCTTA	360
CATGCTGAAA		TGATATGCAC	TATATTCAGT	ATACGTATGT	TTTCCTACTT	420
CTCTTGTAAA		GATCCAACTT	CAGCAATGAA	TTGTGCCTAG	TGGAGAACCT.	480
CTATAGATCT	TAAAAAATGA		AGCAGTGTAT	TACTCACATG	GGTGCAATCT	540
TTAGCCCCAG		AATGTCTTTT	AAAGCCAGAA	GTCACATTTT	ACCAATATGC	600
	ATTGGTGCTT	AGGCTGTATA	TTCAAGCCTG	TTGTCTTAAC	ATTTTGTATA	660
	ACAGAAATTA	TCTGTCATTT	GAGAAGTGGC	TTGACAATCA	TTTGAGCTTT	720
GAAGCAGTCA		ATATGAATGC	TGTCCTAGTG	GTCATAGTAC	CAAGGGCACG	780
TGTCTCCCCT	TGGTATAACT	GATTTCCTTT	TTAGTCCTCT	ACTGCTAAAT	AAGTTAATTT	840
TGCATTTTGC	AGAAAGAAAC	ATTGATTGCT	AAATCTTTTT	GCTGCTGTGT	TTTGGTGTTT	900
TCATGTTTAC	TTGTTTTATA	TTGACTGTTT	TAAGTATGAG	AGGCTTATAG	TGCCCTCCAT	960
TGTAAATCCA	TAGTCATCTT	TTTAAGCTTA	TTGTGTTTAA	GAAAGTAGCT	ATGTGTTAAAI	.020
CAGAGGTGAT	GGCAGCCCTT	CCCTAGCACA	CTGGTGGAAG	AGACCCCTTA	AGAACCTGAC1	080
CCCAGTGAAT	GAAGCTGATG	CACAGGGAGC	ACCAAAGGAC	CTTCGTTAAG	TGATAATTGT1	140
CCTGGCCTCT	CAGCCATGAC	CGTTATGAGG	AAATATCCCC	CATTCGAACT	TAACAGATGC1	200
CTCCTCTCCA	AAGAGAATTA	AAATCGTAGC	TTGTACAGAT	CAAGAGAATA	TACTGGGCAG1	260
AATGAAGTAT	GTTTGTTTAT	TTTTCTTTAA	AAATAAAGGA	TTTTGGAACT	CTGGAGAGTA1	320
AGATATAGTA	TAGAGTTTGC	CTCAACACAT	GTGAGGGCCA	AATAACCTGC	TAGCTAGGCA1	380
GTAATAAACT	CTGTTACAGA	AGAGAAAAAG	GGCCGGGCAC	AGTGGCTTAT	TCCTGTAATC1	440
CCAACACTGT	GGAAGGCCGA	GGCAGGAGGA	TCACTTGAGT	CCAGGAGTTT	GAAACCTACC1	500
TAGGCAACAT	GGTGAAACCT	TGTCTCTACC	AAAATAAAAA	TTAGCTGGGC	ATGGTGGCAC1	560
GTGCCTGTGG	TCCCAGCTAC	TTGGGAGGCT	GAGGTGGGAG	CCTGGGAGGT	CAAGGCTGCA1	620
GTGAGCCATG	ATCATGCCAC	TGCACTCCAT	CCTGGGTGAC	AGCAAGATCT	TGTAAAAAAA1	680
AAAAAAAAA	AAACCAGGAG	TGAAAAAGGA	AAGTAGAAGG	CAGCTGCTGG	CCTAGATGTT1	740
GGTTTGGGAA	TATTAGGTGA	TCCTGTTGAG	ATTCTGGATC	CAGAGCAATT	TCTTTAGCTT1	800
TTGACTTTGC	CAAAGTGTAG	ATAGCCTTTA	TCCAGCAGTA	TTTTAAGTGG	GGAATGCAAC1	860
GTGAGGCCAA	CTGAACAATT	CCCCCGTGG	CTGCCCAGAT	AGTCACAGTC	AAGGTTGGAG1	920
AGTCTCCTTC	CAGCCAGTGA	CCTACCCAAA	CCTTTTGTTC	TGTAAAACTG	CTCTGGAAAT1	
ACCGGGAAGC	CCAGTTTTCT	CACGTGGTTT	CTAGCTTCTT	CAGACTCAGC	CCAAATTAGG2	
AAGTGCAGAA	GCACATGATG	GTGAAAAACC	TAGGATTTGG		GAATGGTATG2	
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GAATCTGAGG GAAGATTTAT GTTTCGTTTT GGAGGATAGC TCAAGTTGAA TTTTCTTTCC2160 AGCCAGTTAC CCTTTCAACC TACCCATACT TTGTACAACT CTTACACAAA TACTTAGATA2220 TTTATTAGAT AGCCCTGAAT TCACTCTAAT TATAAACAGG GAGTGTAAAC TGCCCCCAGA2280 TGTTCCTGGG CTGGGTAAAA GCAGCTGGAG TGAAGCACTC ATTTTCCATA AAGGTAACAA2340 AGGGCAGCTC AGTGGTTACT CAAGCTCAAA AGGGTTTTTT TAAGAGCAAG CATTGGTTAA2400 GTCTGTGTAT ACTGAGTTGG AAGTGATTTC AGCACATTCT TTTTTAGTGG AGTGAAAGTT2460 CTGAAGCCCC CTTTTAACTT CCTCTTGGTT TTTCATTATA ATTGGTAGCC ATCTCATGAA2520 CTGTCTCTGA CTGTTGTCTC TTTGTGGTCA TGTGATTGTG AGCTTGCTTT CTGACTTGCA2580 TTTCTGACTT TATCCTGTTG TTAGGAAGAT AGAAACTAGG TTTTGAAAGA TTACATGATT2640 CAAGCGAGGG ATTTTAAAGT AAAGATGTAT TTATTCTGAA GAATCTAAAA GATAACAGAT2700 TATTTGCTTA TGAAAGAACA ATATAGTCTG GGAATCCCAG AATGTCAAGC CAAAGGTCTA2760 AGAAGTCATC TCCTTCAAAT ACTTTAATAA AGAAGTATTT CGAGGAGATA TCTGTCCAAA2820 AAGGTTTGAC TGGCCTCCAG ATTCCAGTTA TTTTTAAAAA GCAACTTACC ACTAAATCCT2880 TGAGTCTCCA TAGAGTAACA GTAAAGAAAC TGATGTAACA GACTCTCCTC TCAAAGGATC2940 TCCTCTGGAA GAGACTATCA GCGGCAGGAT TCTCCAGGGA AGACCCATCC CCTAGTGCCA3000 GAGCTTGCAT CCTGGAGACT AAAGATTGCA CTTTTTTGTA GTTTTTTGTC CAAATGCAAT3060 CCCATTTCTG TGCCTCTTAG CATGCAGTTA GATTTGGACA AACAAGATTC CTAAGGAATG3120 ACTTTATTAA CTATAATATG GTTACAGCTA TTATATAAAT ATATATTCTG GTTATAGTTC3180 TÄATATGGAG ATGTTGTGTG CAATGCTGGC CTGTGGTGGT CTGTGTÄATG CTTTAACTTG3240 TATGGAGGAG GCCAGGCTCA GAGCTGAGAT GTGGCCTGAA CCTTCCCTGT ATCGATCCTT3300 TAATTTAGAA CTGTCAAGAT GTCACTTTCT CCCCCTCTGC CTTTTAGTGG TATCTGACAT3360 ATACTCAAAA CAGTAATTTC CTGGTCACAT CATTAACTGC TAATTCTGTA TTTATAAAGA3420 ATTTTCAGAT GGACATGTAC AAATTTGAAC TCAAACCATC CCCAGTCCAG ATACAGGGCA3480 GCGTGTAGGT GACCACACA GAGCCTCAGC CTCGGTCCTT CTCAGCCGTC GGGATAGGAT3540 CCAGGCATTT CTTTTAAATC TCAGAGGTAG CAGTAAACTT TTCAGTATTG CTGTTAGCAA3600 GTGTGTGTTT GCCAATAGAT ACCCATTATA CTAATGTGCC AAGTAAATGT TCATTGCACA3660 TCTGCTTCCA CTGTGTTCCC ACGGGTGCCA TGAAGTGTGT GAGGAGCCCC TCATCTGGAG3720 GGATGAGTGC TGCGTTGACT ACTGCTATCA GGATTGTGTT GTGTGGAATA TTCATCTACA3780 TAAATTTTAT ATGCACAGTA ATTTCCCTTT TTATATGTCA AGTAACTATT TGTAAAAGTT3840 ATACTCACAA ATTATTATAA TGATTACTAA TATATTTTTT CCATGTTTCA TTGCCTGAAT3900 AAAAACTGTT TACCACTGTT AAAAAAAAAA AAAAAAAAA AAAAAAATGG GAAAAAAAG3960 CTGGGGGGG GGCCCGGTAG CC

(2) INFORMATION ON SEQ ID NO. 402:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1876 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

CTCTTGGATC CCCTGGACCA CTGGGCATAC TCGCCATCCT CTTCCGGAGA TCTGGGCAGT TCGCCTGCAT TAGAGCTCCT GATTGAGATT CAGTGCATCA GCCGTGCTAT CCATCACGTC 120 CACACCTCTG TGCCCACTCT TGAAGCTGTT GGGAAATATT CAGCAATGTC CGCATCAACT 180 TGCAGAAGAA TATAAATGAC ATTTCAAGGA TAGAAGATAC CTGATTTTTT TTCCTTTTAA 240 TTTTCCTGGT GCCAATTTCA AGTTCCAAGT TGCTAATACA GCAACAATTT ATGAATTGAA 300 TTATCTTGGT TGAAAATAAA AAGATCACTT TCTCAGTTTT CATAAGTATT ATGTCTCTTC 360 TGAGCTATTT CATCTATTTT TGGCAGTCTG AATTTTTAAA ACCCATTTAA ATTTTTTTCC 420 TTACCTTTTT ATTTGCATGT GGATCAACCA TCGCTTTATT GGCTGAGATA TGAACATATT 480 GTTGAAAGGT AATTTGAGAG AAATATGAAG AACTGAGGAG GAAAAAAAAA AAAAAGAAAA 540 GAACCAACAA CCTCAACTGC CTACTCCAAA ATGTTGGTCA TTTTATGTTA AGGGAAGAAT 600 TCCAGGGTAT GGCCATGGAG TGTACAAGTA TGTGGGCAGA TTTTCAGCAA ACTCTTTTCC 660 CACTGTTTAA GGAGTTAGTG GATTACTGCC ATTCACTTCA TAATCCAGTA GGATCCAGTG 720 ATCCTTACAA GTTAGAAAAC ATAATCTTCT GCCTTCTCAT GATCCAACTA ATGCCTTACT 780 CTTCTTGAAA TTTTAACCTA TGATATTTC TGTGCCTGAA TATTTGTTAT GTAGATAACA 840 AGACCTCAGT GCCTTCCTGT TTTTCACATT TTCCTTTTCA AATAGGGTCT AACTCAGCAA 900 CTCGCTTTAG GTCAGCAGCC TCCCTGAAGA CCAAAATTAG AATATCCATG ACCTAGTTTT 960 CCATGCGTGT TTCTGACTCT GAGCTACAGA GTCTGGTGAA GCTCACTTCT GGGCTTCATC1020 TGGCAACATC TTTATCCGTA GTGGGTATGG TTGACACTAG CCCAATGAAA TGAATTAAAG1080 TGGACCAATA GGGCTGAGCT CTCTGTGGGC TGGCAGTCCT GGAAGCCAGC TTTCCCTGCC1140 TCTCATCAAC TGAATGAGGT CAGCATGTCT ATTCAGCTTC GTTTATTTTC AAGAATAATC1200 ACGCTTTCCT GAATCCAAAC TAATCCATCA CCGGGGTGGT TTAGTGGCTC AACATTGTGT1260 TCCCATTCA GCTGATCAGT GGGCCTCCAA GGAGGGGCTG TAAAATGGAG GCCATTGTGT1320 GAGCCTATCA GAGTTGCTGC AAACCTGACC CCTGCTCAGT AAAGCACTTG CAACCGTCTG1380 TTATGCTGTG ACACATGGCC CCTCCCCTG CCAGGAGCTT TGGACCTAAT CCAAGCATCC1440 CTTTGCCCAG AAAGAAGATG GGGGAGGAGG CAGTAATAAA AAGATTGAAG TATTTTGCTG1500 GAATAAGTTC AAATTCTTCT GAACTCAAAC TGAGGAATTT CACCTGTAAA CCTGAGTCGT1560 ACAGAAAGCT GCCTGGTATA TCCAAAAGCT TTTTATTCCT CCTGCTCATA TTGTGATTCT1620 GCCTTTGGGG ACTTTTCTTA AACCTTCAGT TATGATTTTT TTTTCATACA CTTATTGGAA1680 CTCTGCTTGA TTTTGGCCTC TTCCAGTCTT CCTGACACTT TAATTACCAA CCTGTTACCT1740 ACTTTGACTT TTTGCATTTA AAACAGGACA CGGGGCAGGG AGAAAAGGGT TTTAGTTTT1800 AAACCCGGTG GTTACCATAA CGCGGGAAAA GGTGGCCCAT ACGGGGCAAA CGTTTTTGAA1860 1876 AGGTTAAGGG TATTTT

(2) INFORMATION ON SEQ ID NO. 403:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1216 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

TCTGTTCTGT GGACAACTGT TACTGTTCTT CCGTGGCCAA CCATGGCGGC CACCAGCCCT 60 ACCCCGCTC CGGCCACTTT CCCTGGACAG TGCCCTCGCA GGAGTACTCA CACCCGCTCC 120 CGCCCACACC CTCCGTCCCC CAGTCCCTTC CCAGCCTGGC GGTCAGAGAC TGGCTTGACG 180 CCTCCCAGCA GCCCGGCCAC CAGGATTTCT ACAGGGTGTA TGGGCAGCCG TCCACCAAAC 240 ACTACGTGAC GAGCTAACGC CACGCAGGCG GCGGGGCGCT GGGGAATCTT CCTCCCCAGC 300 CCCCGGGCTC GGGAGTTATG CATCCAGAGA CCTGCCCTTC TACCTTCCTC GCCTCCCCTC 360 TTECTCATTC CATTGCCCCA GGTCTTTTCC TTTTGGATTT TGTTTTGGTT TTGGCTTTGT 420 TTTTGATTTT TTTTTATTAT GAATCTCCTG GACGCAGAGG TGACAGTGGG AGCTGGCCTG 480 GGCCAGGACG GCAGGTGGCC CTGGAGATGG GAAAGTGTCT GTGTCGAGGC GCTGAGCTCT 540 CTCTCTGTTT CTCCTTTTTT CCTCTACTCC TTCCCCTTCA CACCCCCGTG GCTGGAAGGA 600 ACCTCGGCTT CCCTGAAAGC TTGGGGGTCC CACCCTTCTT ACCCCACCCG GGAGGAACGC 660 CCAGGGCCCC GGGCTTGTTT CTCCTCTTGT TTTCCTTTTG GGCAGTTTGA TCACTGATCG 720 AGTAAGGAAT GACCTTTAGA TTGTGCGACT TTTGTTTTTG TTTTTTTAAA TTTTTTTAAA 780 CCAAGAATGA TTTCTCCTGC TTCCTTCTC TCACCATCTT CCCAGACGGA GTTCAAAGGC 840 CACTTCTCAA GCAGCTTTTG GCACCTTCAG CCTCAGAGTG GAATCTTTTA AAGACAGGAC 900 CCCTATGTCC AGGAAAGGG AAAAGGAACT TTGCCAATGA TAGTGACCAC AGCAAAAGCA 960 ATAAAATAAT AAAATAAAAA ACAATAGCAC AGCCCTTGTT GAGGTCAGCA GGGAGGAGGG1020 GCTGCCCGGA GTTGGGTCCT TGCCTGGATT TTGACACAGC AACTTCCTGT AGTGAGCACT1080 TTGTATGAAT CGTGGACTTC CTGTTCTCAA GGCGCAGGTA TTTATTCTGT ATCTGTCTAG1140 AGCACACCC AAAATCCAAC CTTCTAATAA ACATGATGGC GCAGTCCCAA AAAAAAGAAA1200 1216 CAGAAGAAGA AAAGGG

(2) INFORMATION ON SEQ ID NO. 404:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 271 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

RPRAGASIST LAGLSLKEGE DQKEIKIEPA QAVDEVEPLP EDYYTRPVNL TEVTTLQQRL 60 LQPDFQPVCA SQLYPRHKHL LIKRSLRCRK CEHNLSKPEF NPTSIKFKIQ LVAVNYIPEV120 RIMSIPNLRY MKESQVLLTL TNPVENLTHV TLFECEEGDP DDINSTAKVV VPPKELVLAG180 KDAAAEYDEL AEPQDFQDDP DIIAFRKANK VGIFIKVTPQ REEGEVTVCF KMKHDFKNLA240 APIRPIEESD QGTEVIWLTQ HVELSLGPLL P

- (2) INFORMATION ON SEQ ID NO. 405:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

DLKQDQGKQK ICIFLKSLGH LLTILLQKTR CSWWSTLSSF ILENIIEIKV SNPTPGYQVK 60 TASLLLGQNC GLLAELFYGL QSKWSYLTHH MTKVLNLVRG KVLNIQFWIQ EIIIVNFPFK120 133 SMERMLVENI LKI

(2) INFORMATION ON SEQ ID NO. 406:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

RGPGHLLKPN GGPPMKLGYG RNLDISPRLP LNRETVKRSI RFHRFWPLIP NSFPHNSVFL60 VSMKCLESHR KPVKIFLKKK KPQKTDHLSI QWTSI

- (2) INFORMATION ON SEQ ID NO. 407:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

YLSLCPCWPG NFFQWCLLEE VFSSCHFKKI KLEIEYGWHD CTLLVLLFFY SSVPL 55

(2) INFORMATION ON SEQ ID NO. 408:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

LQEAPCGEHG RHLHKSAMRR DTESELHHQR QVQGAETVGS GQGSAAFSGP SPYARGPGPD 60 LPLLGGQHLS IRRWFKCVTM SQCVLELPFS NANLPSLHIS PHPWTRFCVS ESGNLLKRGG120 STPGLLV

(2) INFORMATION ON SEQ ID NO. 409:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

KGVGLLIMGG QGQVLGHRER VRRMLQTPAH CPRSPLPAPA SDGAALIPCL SSLQIYEGAY60 HVLHKELPEV TNSVFHEINM WVSORTATAG TASPP 95

(2) INFORMATION ON SEQ ID NO. 410:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 296 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

VVRLAPTEGH YVCTVISHAH EVRQMQELRR VRSGVMSEKD HMVTMHDVLD AQWLYDNHKD 60 ESYLRRVVYP LEKLLTSHKR LVMKDSAVNA ICYGAKIMLP GVLRYEDGIE VNQEIVVITT120 KGEAICMAIA LMTTAVISTC DHGIVAKIKR VIMERDTYPR KWGLGPKASQ KKLMIKQGLL180 DKHGKPTDST PATWKQEYVD YSESAKKEVV AEVVKAPQVV AEAAKTAKGS EESESESDET240 PPAAPQLIKK EKKKSKKDKK AKAGLESGAE PGDGDSDTTK KKKKKKKAKE VELVSE 296

(2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 280 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

RDQGGGSLRS FPRLWTGRHD AVQGNMADAE VIILPKKHKK KKERKSLPEE DVAEIQHAEE 60
FFIKPESKVA KLDTSQWPLL LKNFDKLNVR TTHYTPLACG SNPLKREIGD YIRTGFINLD120
KPSNPSSHEV VAWIRRILRV EKTGHSGTLD PKVTGCLIVC IERATRLVKS QQSAGKEYVG180
IVRLHNAIEG GTQLSRALET LTGALFQRPP LIAAVKRQLR VRTIYESKMI EYDPERRLG1240
FWVSCEAGTY IRTLCVHSDQ SRARGTSDAG ASEGSFWSHE

- (2) INFORMATION ON SEQ ID NO. 412:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

RHPHPEGVMG FSRGCGSASS ILWKPDHCPW QRFPGHQEFE EERLRPAGMH GTQRGRGGQV 60
DPAAHCPGAH GETHLPRPDQ REDHGHGGAT TFSLNCSAAG TPTPSLVWVL PNGTDLQSGQ120
QLQRFYHKAD GMLHISGLSS VDAGAYRCVA RNAAGHTERL VSLKVGLKPE ANKQYHNLVS180
IINGETLKLP CTPPGAGQGR FSWTLPNGMH LEGPQTLGRV SLLDNGTLTV REASVFDRGT240
YVCRMETEYG PSVTSIPVIV IAYPPRITSE PTPVIYTRPG NTVKLNCMAM GIPKADITWE300
LPDKSHLKAG VQARLYGNRF LHPQGSLTIQ HATQRDAGFY KCMAKNILGS DSKTTYIHVF360

(2) INFORMATION ON SEQ ID NO. 413:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 314 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

EEGDYTCFAE NQVGKDEMRV RVKVVTAPAT IRNKTYLAVQ VPYGDVVTVA CEAKGEPMPK 60
VTWLSPTNKV IPTSSEKYQI YQDGTLLIQK AQRSDSGNYT CLVRNSAGED RKTVWIHVNV120
QPPKINGNPN PITTVREIAA GGSRKLIECK AEGIPTPRVL WAFPEGVVLP APYYGNRITV180
HGNGSLDIRS LRKSDSVQLV CMARNEGGEA RLILQLTVLE PMEKPIFHDP ISEKITAMAG240
PQHSASTALP RGPRHPAWCG SFPMAPICRV DSSCSASTTR LTACYTLAVS PRWTLGPTAA300
WPAMPLATRR GWSP 314

- (2) INFORMATION ON SEQ ID NO. 414:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

RPVPAKLNPR SWPRTAGALP LRPPPLTMAV FHDEVEIEDF QYDEDSETYF YPCPCGDNFS 60 ITKEDLENGE DVATCPSCSL IIKVIYDKDQ FVCGETVPAP SANKELVKC 109

- (2) INFORMATION ON SEQ ID NO. 415:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

YAKSTATSHG NLTLTPTWNA ISLALSKHKQ KLRYRNITCS DLAKSFKHST YYTGMLCSSH 60 SVTNFTSFGC FSFHLVLTSK EYAEYKKSPH SFITSFWTFF LVH 103

- (2) INFORMATION ON SEQ ID NO. 416:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids

 - (B) TYPE: Protein(C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - ORIGIN (vi) (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

YTMXIIYFTR XILYXQGGIL KYNTPGXSFL LYIMIVSFHI SWXLXXGKGT XKSIFIYIKT 60 KXXQXRLXPP KCLVSLENNM NEXXKMNQIT WXTHRRXNKX AQEIKSCFKL GHIKGKKGSE120 RRVRKISSQA TKNLXRRQPP NXIR

- (2) INFORMATION ON SEQ ID NO. 417:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

LILMGRLIYN XNYLFYKXDS IHXGRHLEVQ YTRXFISSLH YDCEFPYKLX TXHXKGNXKI60 HFYIHKNKTX PXET

- (2) INFORMATION ON SEQ ID NO. 418:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

YPFFTLCQRN RVFDISSYVK EMLQNVNCFK LKLPLKRPRY IYLIVYIMFN ICQSILQVCS 60 FISIKYGYYV AQLLKWYCIV YICTPNNIVC TFCFLYCICA GFFRLYQCNL CLLRYVQKMS120 I

- (2) INFORMATION ON SEQ ID NO. 419:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

FFFFFFFFF FQRIHFFFFF FFFFFGKNVI YLHCFHSSTV VLGLNISITL LFPIYILLEY 60 YYKYNIQFKK TYGETQLMFF SPLYRLLSII RLQWKFIWTF SVHILKGRDY TDKA 114

(2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 765 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVIKNL KKTPNFPSSV 60
LFMKVFLPKE ELYMPPLVIK VIDHRQFGRK PVVGQCTIER LDRFRCDPYA GKEDIVPQLK120
ASLLSAPPCR DIVIEMEDTK PLLASKLTEK EEEIVDWWSK FDASSGEHEK CGQYIQKGYS180
KLKIYNCELE NVAEFEGLTD FSDTFKLYRG KSDENEDPSV VGEFKGSFRI YPLPDDPSVP240
APPRQFRELP DSVPQECTVR IYIVRGLELQ PQDNNGLCDP YIKITLGKKV IEDRDHYIPN300
TLNPVFGRMY ELSCYLPQEK DLKISVYDYD TFTRDEKVGE TIIDLENRFL SRFGSHCGIP360
EEYCVSGVNT WRDQLRPTQL LQNVARFKGF PQPILSEDGS RIRYGGRDYS LDEFEANKIL420
HQHLGAPEER LALHILRTQG LVPEHVETRT LHSTFQPNIS QGKLQMWVDV FPKSLGPPGP480
PFNITPRKAK KYYLRVIIWN TKDVILDEKS ITGEEMSDIY VKGWIPGNEE NKQKTDVHYR540
SLDGEGNFNW RFVFPFDYLP AEQLCIVAKK EHFWSIDQTE FRIPPRLIIQ IWDNDKFSLD600
DYLGFLELDL RHTIIPAKSP EKCRLDMIPD LKAMNPLKAK TASLFEQKSM KGWWPCYAEK660
DGARVMAGKV EMTLEILNEK EADERPAGKG RDEPNMNPKL DLPNRPETSF LWFTNPCKTM720
KFIVWRRFKW VIIGLLFLLI LLLFVAVLLY SLPNYLSMKI VKPNV 765

- (2) INFORMATION ON SEQ ID NO. 421:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 289 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60
FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFLGFPG120
CDVERRAWWP QTLGENIHPH LKFSLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSKPLFRG180
PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240
NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIIID RNFQVFFLR 289

(2) INFORMATION ON SEQ ID NO. 422:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

FFLYSFSSDN HDFRSFKTIY LAFVSGGELA ISLLKPAIIV NLRTGLSWGS EGKELFEQMC60 VGGTGFHPTA KLVLLEISFY NTKISLCQRF 90

- (2) INFORMATION ON SEQ ID NO. 423:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

TPSGSSWRTY LSRRNSKGER TGPPLIPMTL PPGPLPTTCG NSQKINSSCN FSGDIAQTHI60 TGDAHFFSIR DSQSEETPCV A 81

- (2) INFORMATION ON SEQ ID NO. 424:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

ENWASRYFQS SFTEQKVWVG HWLEGDSPTL TVTIWAATGG IVQLASRCIP HLKYCWIKAI 60 YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLFH SWFFFFFFLQ DLAVTQDGVQ120 WHDHGSLQP

(2) INFORMATION ON SEQ ID NO. 425:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

EAQKWDCIWT KNYKKVQSLV SRMQALALGD GSSLENPAAD SLFQRRSFER RVCYISFFTV 64 TLWRLKDLVV SCFLKITGIW RPVKPFWTDI SSKYFFIKVF EGDDFLDLWL DILGFPDYIV120 LS

- (2) INFORMATION ON SEQ ID NO. 426:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

RFKKSPQRQN HNMSRRNKKL LDIPGSFLYD SGLQVKFLSL SSEEFELIPA KYFNLFITAS 60 SPIFFLGKGM LGLGPKLLAG GGAMCHSITD GCKCFTEQGS GLQQL 105 (2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

EKYEELRRKK KKKKRTNNLN CLLQNVGHFM LREEFQGMAM ECTSMWADFQ QTLFPLFKEL60 VDYCHSLHNP VGSSDPYKLE NIIFCLLMIQ LMPYSS

- (2) INFORMATION ON SEQ ID NO. 428:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGIN
 - (A) ORGANISM: HUMAN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

RKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNKIQKEK 60 TWGNGMRKRG GEEGRRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVFG GRLPIHPVEI120 LVAGLLGGVK PVSDRQAGKG LGDGGCGRER V

- (2) INFORMATION ON SEQ ID NO. 429:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids

 - (B) TYPE: Protein (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLLDFVL VLALFL1FFY 60 YESPGRRGDS GSWPGPGRQV ALEMGKCLCR GAELSLCFSF FPLLLPLHTP VAGRNLGFPE120 SLGVPPFLPH PGGTPRAPGL FLLLFSFWAV 150

(2) INFORMATION ON SEQ ID NO. 430:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 285 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

SWRTGGWAYA GDRLENKTSV SVASWASSLN ARMDNRFATA FVIACVLSLI STIYMAASIG 60
TDFWYEYRSP VQENSSDLNK SIWDEFISDE ADEKTYNDAL FRYNGTVGLW RRCITIPKNM120
HWYSPPERTE SFDVVTKCVS FTLTEQFMEK FVDPGNHNSG IDLLRTYLWR CQFLLPFVSL180
GLMCFGALIG LCACICRSLY PTIATGILHL LAGLCTLGSV SCYVAGIELL HQKLELPDNV240
SGEFGWSFCL ACVSAPLQFM ASALFIWAAH TNRKEYTLMK AYRVA 285

(2) INFORMATION ON SEQ ID NO. 431:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

LCPFWWAIPM HVFGYGDTPS PQSHCAIVSK KCIIISLFIC LITNEFIPDA FIQITGIFLN 60 WTSIFIPEVC ANGGCHVDGG NEAKHTSNYK CCSKTVIHSG IQTARPGCYG DRGLVL 116